

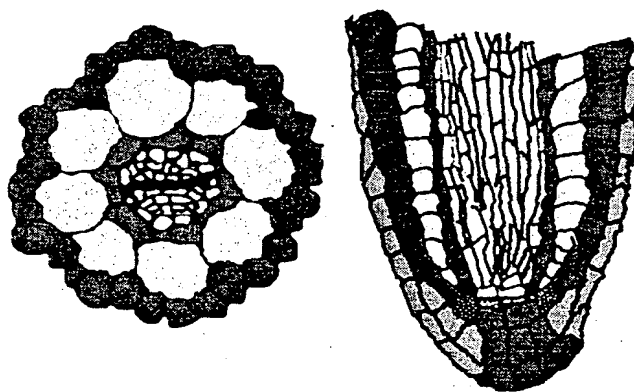


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EPIDERMIS

CORTEX

ENDODERMIS

PERICYCLE

ROOT CAP



VASCULAR TISSUE

CORTEX/ENDODERMAL INITIAL

EPIDERMAL/ROOT CAP INITIAL

QUIESCENT CENTER

FIG.1A



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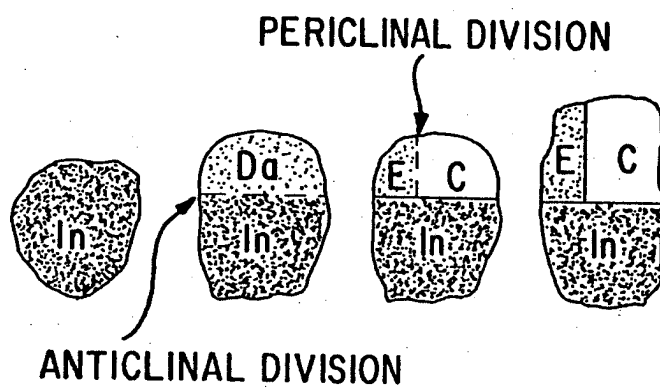


FIG.1B



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FIG.2A



FIG.2B

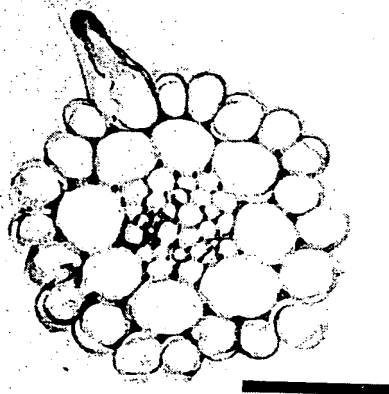
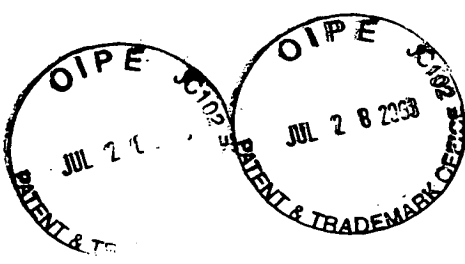


FIG.2C



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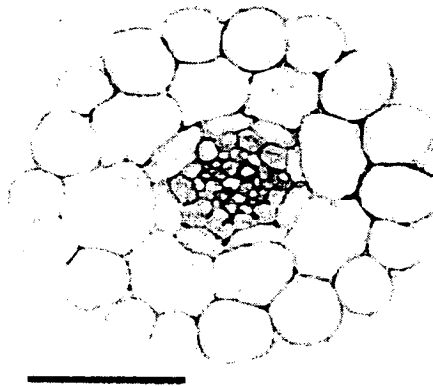


FIG.2D

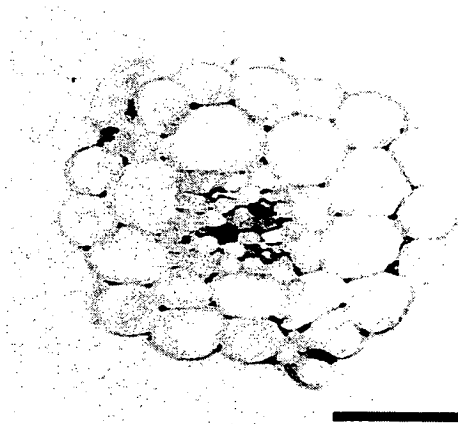


FIG.2E

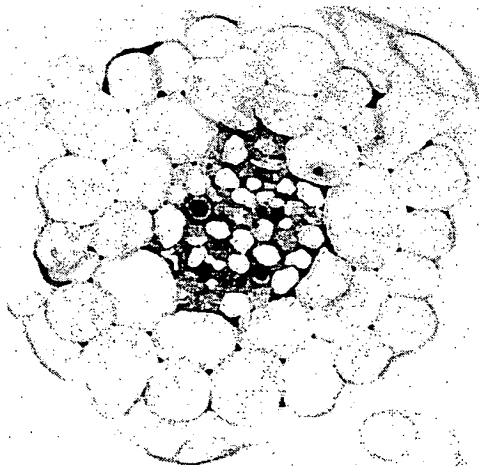


FIG.2F

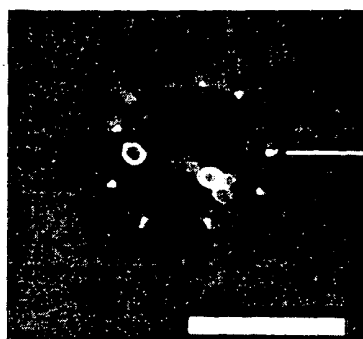


FIG. 3A

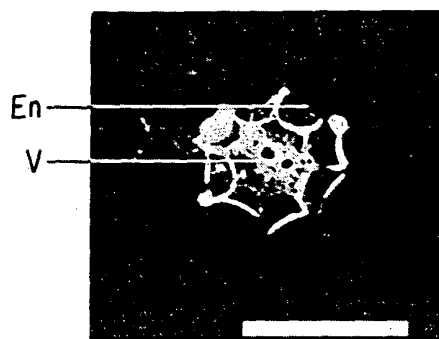


FIG. 3D

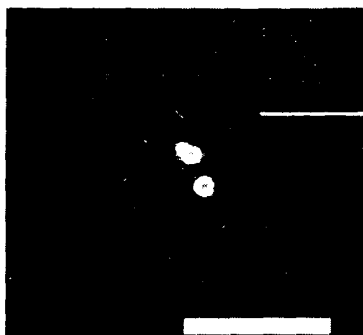


FIG. 3B

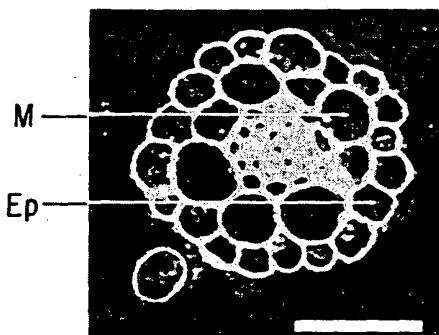


FIG. 3E

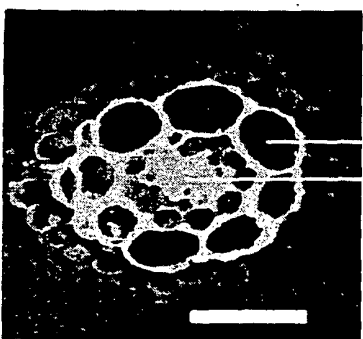


FIG. 3C

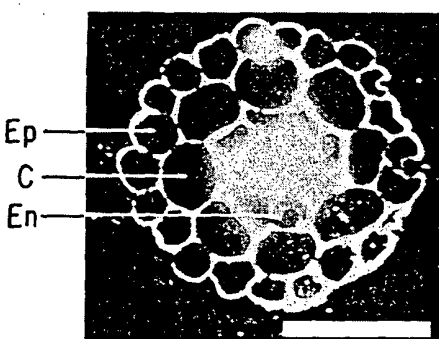


FIG. 3F

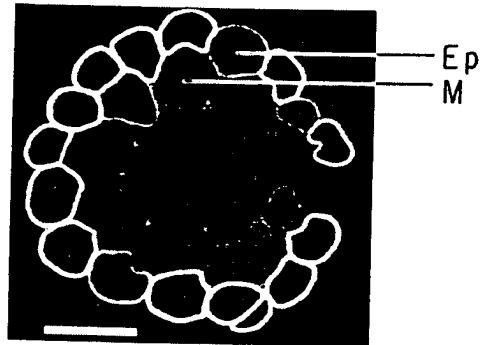


FIG. 4A

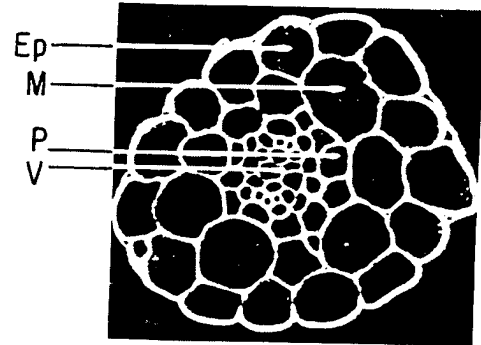


FIG. 4D

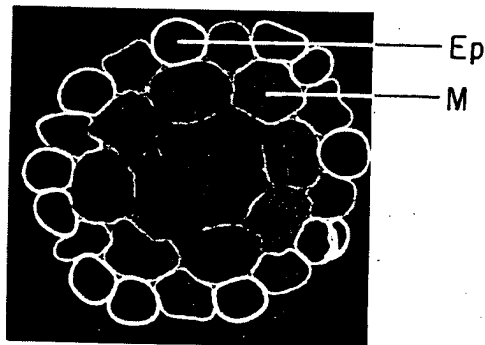


FIG. 4B

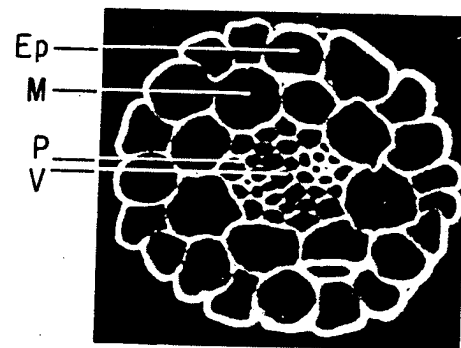


FIG. 4E

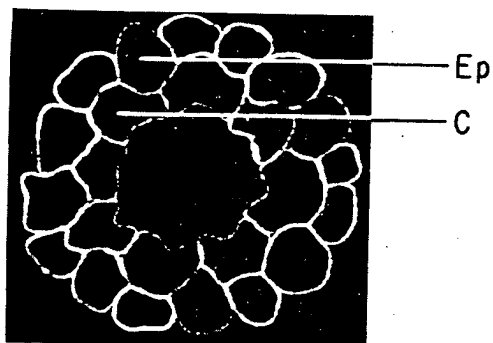


FIG. 4C

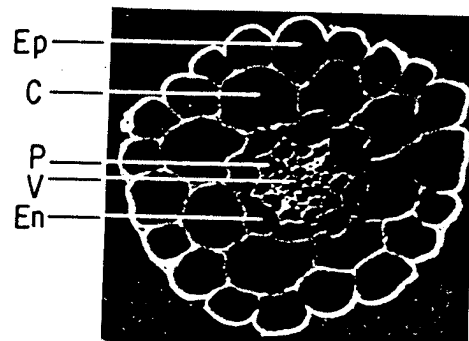


FIG. 4F



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CCTATTATAACCATGCAATCTCAGCACCACAACCCCTTCAATCTCCATGGCGGAA TCGCGCGATTTCACACCGTCTCAAGCTCCCTCATAGCTCTGAGAACAACCTCTCCCGT
M A E S G D F N G G Q P P P H S P L R I I S S G 24
AGTACGACGACAACCGTGGTCCCTCCCTCCCTCCCTTCTAGTATGGTGAGAAAAGATTAGCTTCGAGATGCTTCAACCTGACTACACAACAACCTCTCTGCTCT
S S S N N R G P P P P P P L V H V R K R L A S E M S S H P D Y H N S S R P 64
CCTCGCGGTGCTCTCACCCTTCTTGACTCCAACCTACATACTGTACAGCACACAACCGTCTCTTACGCGCGCGGTACTGTATCTTCTCAACCAACCCACCACCTCTCTGTTGT
P R R V S H L L D S N Y N I V I P Q Q P P S L I A A A I V S S Q P N P L S V C 104
GGCTTCTCGGTCTTCCCGTTTTCCTTCAGACCGTGGTGGTCCGAATGTTATGATGTCGGTACAAACCAATGGATCAAGACTCTTCACTTCTTCTGCTTCACTGTATGGGTGAC
G F S G L P V F P S D R G G R N V M S V Q P M D Q D S S S S A S P I V W V D 144
GCCATTATCAGAGACCTTATCCATTGCTCAACTTCAGTCTCTATTCTCAACTTATCCAAAACGTTAGAGACATTATCTTCCCTTGTAAACCCAAATCTCGGTGCTCTTCTTGAATACAGG
A I I R D L I H S S I S V S I P Q L I Q N V R D I I F P C H P N L G A L L E Y R 184
CTCGATCTCTCATGCTCTCTGATCCCTTCTCTGACCTTCTCTCAAACTTTCGAACCTCTCTATCAGATCTTCCAAATCTCTTCTCCCTCCACAACGACGACGACCCAA
L R S L M L L D P S S S S D P S P Q I F E P L Y Q I S N N P S P P Q Q Q Q Q H Q 224
CAACAACAACAACAGCATAAGCCTCTCTCTCTCGATTTCAGCAGCAAGAAGAAAATTCTTACCGATGCACCCAGCAGACAGTACGCGCCACTGTTCCCGCGCTCCAA
Q Q Q Q Q H K P P P P I Q Q Q E R E N S S I D A P P Q P E I V I A I V P A V Q 264
ACAAATACCGCGAGGCTTTAAGAGAGAGGAAGAGATTAAAGGAGAGAGCAAGCAAGAGGATTACACCTTCTCACATTGCTGCTACAGTGTGCTGAAGCTCTCTGCTGAT
I N I A E A L R E R K E E I K R Q K Q D E E G L H L L T L L Q C A E A V S A D 304
AATCTCGAAGAGCAACAGCTTCTTCTGAGATCTCTCAGTTATCAACTCTTACGGACCTCAGCGCAGAGTAGTCTTACTTCTCGGAAGCTATGTGCGGAGATTACTCAAC
N L E E A N K L L L E I S Q L S T P Y G T S A Q R V A A Y F S E A M S A R L L N 344

FIG.5A-1



TCGTCTCGGAATTTACGGGCTTTGCTTACGGTGGATGCTCAACGCGATAGCTTGAATAATGGTCTCTGCTTTCAGGCTCTTTAATGGATAAGCCCTTTAGTGAATTCACAC
S C L G I Y A A L P S R W M P Q T H S L K M V S A F Q V F N G I S P L V K F S H 384

TTTACAGCGAATCAGCGGATTCAAGAGCATTTGAGAAGAAGACAGTGACACATCATTTGACTTGGACATCATGACGCGACTTCAATGGCCTGGTTTATTCACACATTTCTTCTCTAGA
F T A N Q A I Q E A F E K E D S V H I I D L D I M Q G L Q W P G L F H I L A S R 424

CCTGGAGGACCTCCACAGCTGCGACTCAAGGACTTGGTACTTCCATGGAAGCTCTTCAGGCTACAGGAAAGCTCTTTCGGAATTCACAGATAAGCTTCCCTGCTTTTGAGTTCTGCG
P G G P P H V R L T G L G T S M E A L Q A T G K R L S D F T D K L G L P F E F C 464

CCTTAGCTGAGAAAGTTGGAACCTTGACACTGAGAGACTCAATGTGAGGAAAGGGAAGCTGTGGCTGTTCAACATTCCTTTTATGATGTCACGTGCTCTGATGACACAC
P L A E K V G N L D T E R L N V R K R E A V A V H W L Q H S L Y D V T G S D A M 504

ACTCTCTGTTACTCCAAAGGTAAATAAACATTACCTTTTAATCAGCTCTTTAICATATAATTTAAGATTATATAGGAAGATATGTTCTAAAAAGCTGGCTTTTTCGTTAATGA
T L W L L Q R 511

TTCCGGAATGAACAGATTAGCTCCTAAAGTTCTGACAGTAGTGGAGCAAGATTGACCCACGCTGGTTCTTCTTAGGAAGATTGTAGAGGCAATACATTACTCTGCACTCTTTGA
L A P K V V T V V E Q D L S H A G S F L G R F V E A I H Y Y S A L F D 546

CTCACTGGGAGCAAGCTACGGCGAAGAGAGTCAAGAGAGACACATGTGTCGAACAGCAGCTATTATCGAAGAGAGATACGGAATGTATTAGCGGTTGAGGACCATCGACAGCGGTGAAGT
S L G A S Y G E E S E E R H V V E Q Q L L S K E I R N V L A V G G P S R S G E V 586

GAGTTTGAGAGCTGCAGGGAGAAAATGCAACAATGTGGGTTTAAAGGTATATCTTTAGCTGGAATGACAGCTACACAGGAGCTCTACTGTGGGAATGTTTCCCTGGGATGGTTACAC
K F E S W R E K M Q Q C G F K G I S L A G N A A T Q A T L L L G H F P S D G Y T 626

TTTGGTTGATGATAATGCTACACTTAAGCTTGGATGGAAGATCTTTCGTTACTCAGCTTTCAGCTTGGACGCTGCTTCTAGTTTCTCTCTTTTTCACAAACAATGTCGCCATA
L V D D N G T L K L G W K D L S L L T A S A W T P R S STOP 653

2163
AAT

FIG.5A-2

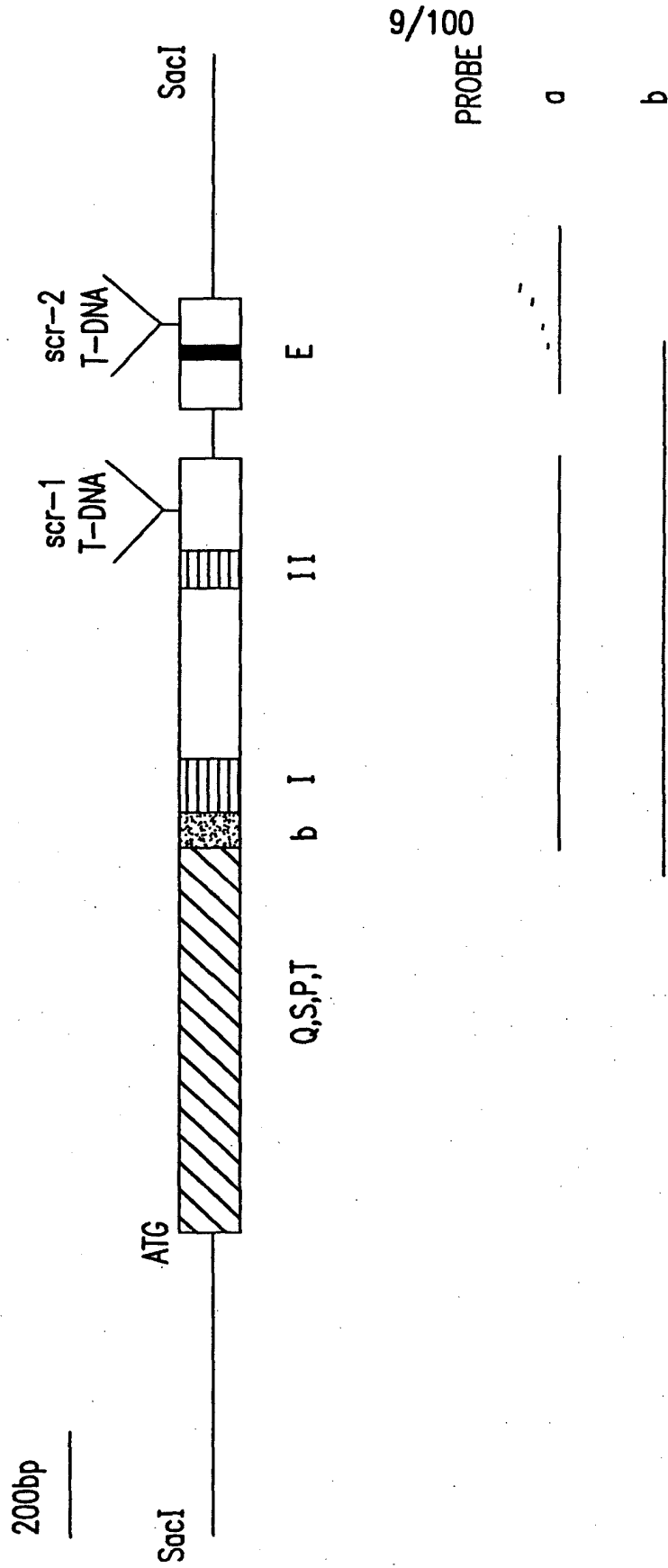


FIG.5B



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SCR bZIP-like domain	PAVQTNTAEALRERKEEIKRQKQ	1
	:	D
GCN4 (yeast)	LKRARNTAAARRSRARKLQRMKQ	L
TGA1 (Arabidopsis)	RRLAQNREAARKSRLRKKAYVQQ	L
C-Fos (mouse)	IRRERNKMAAAKCRNRRRELTDT	L
c-JUN (human)	RKRMRNRIAASKCRKRKLERIAR	L
CREB (human)	VRLMKNREAARECRRKKKEYVKC	L
Opaque-2 (maize)	KRKESNRESARRSRYRKAHLKE	L
OBF2 (maize)	MRQIRNRDSAMKSREKKSYIKD	L
RAF-1 (rice)	RRMVSNRESARRSRKKKQHLAD	L

FIG.5C



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SCR VHIID domain	
SCR	AFEKEDSVHIIDLDIMQGLQWPGLFHILASRPGGPPHVRLTGL ¹
F13896	AVKNESFVHIIDFQISQGGQWVSLIRALGARPGGPPNVRTGI
Z37192	AMEGEKTVHVIDLDASEPAQWLALLQAFNSRPEGPPHLRITGV
Z25645	AIKGEEVHIIDFDINQGNQYMTLIRSA
D41474	IHVIDFXLGVGGQWASFLQELAHRRG
T18310	VHIIXFXLMQGLQWPALMDVFSARKGGPPKLRITGI

FIG.5D

MetAlaGluSerGlyAspPheAsnGlyGlnProProHisSerProLeuArgThr
ThrSerSerGlySerSerSerSerAsnAsnArgGlyProProProProProPro
LeuValMetValArgLysArgLeuAlaSerGluMetSerSerAsnProAspTyrAsnAsn
SerSerArgProProArgArgValSerHisLeuLeuAspSerAsnTyrAsnThrValThr
ProGlnGlnProProSerLeuThrAlaAlaAlaThrValSerSerGlnProAsnProPro
LeuSerValCysGlyPheSerGlyLeuProValPheProSerAspArgGlyGlyArgAsn
ValMetMetSerValGlnProMetAspGlnAspSerSerSerSerAlaSerProThr
ValTrpValAspAlaIleIleArgAspLeuIleHisSerSerThrSerValSerIlePro
GlnLeuIleGlnAsnValArgAspIleIlePheProCysAsnProAsnLeuGlyAlaLeu
LeuGluTyrArgLeuArgSerLeuMetLeuLeuAspProSerSerSerSerAspProSer
ProGlnThrPheGluProLeuTyrGlnIleSerAsnAsnProSerProProGlnGlnGln
GlnGlnHisGlnGlnGlnGlnHisLysProProProProIleGlnGlnGln
GluArgGluAsnSerSerThrAspAlaProProGlnProGluThrValThrAlaThrVal
ProAlaValGlnThrAsnThrAlaGluAlaLeuArgGluArgLysGluGluIleLysArg
GlnLysGlnAspGluGlyLeuHisLeuLeuThrLeuLeuGlnCysAlaGluAla
ValSerAlaAspAsnLeuGluGluAlaAsnLysLeuLeuGluIleSerGlnLeuSer
ThrProTyrGlyThrSerAlaGlnArgValAlaAlaTyrPheSerGluAlaMetSerAla

FIG. 5E-1



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FIG. 5E-2

ArgLeuLeuAsnSerCysLeuGlyIleTyrAlaAlaLeuProSerArgTrpMetProGln
ThrHisSerLeuLysMetValSerAlaPheGlnValPheAsnGlyIleSerProLeuVal
LysPheSerHisPheThrAlaAsnGlnAlaIleGlnGluAlaPheGluLysGluAspSer
ValHisIleAspLeuAspIleMetGlnGlyLeuGlnTrpProGlyLeuPheHisIle
LeuAlaSerArgProGlyGlyProProHisValArgLeuThrGlyLeuGlyThrSerMet
GluAlaLeuGlnAlaThrGlyLysArgLeuSerAspPheThrAspLysLeuGlyLeuPro
PheGluPheCysProLeuAlaGluLysValGlyAsnLeuAspThrGluArgLeuAsnVal
ArgLysArgGluAlaValAlaValHisTrpLeuGlnHisSerLeuTyrAspValThrGly
SerAspAlaHisThrLeuTrpLeuLeuGlnArgLeuAlaProLysValValThrValVal
GluGlnAspLeuSerHisAlaGlySerPheLeuGlyArgPheValGluAlaIleHisTyr
TyrSerAlaLeuPheAspSerLeuGlyAlaSerTyrGlyGluGluSerGluGluArgHis
ValValGluGlnGlnLeuLeuSerLysGluIleArgAsnValLeuAlaValGlyGlyPro
SerArgSerGlyGluValLysPheGluSerTrpArgGluLysMetGlnGlnCysGlyPhe
LysGlyIleSerLeuAlaGlyAsnAlaAlaThrGlnAlaThrLeuLeuLeuGlyMetPhe
ProSerAspGlyTyrThrLeuValAspAspAsnGlyThrLeuLysLeuGlyTrpLysAsp
LeuSerLeuThrAlaSerAlaTrpThrProArgSerSTOP

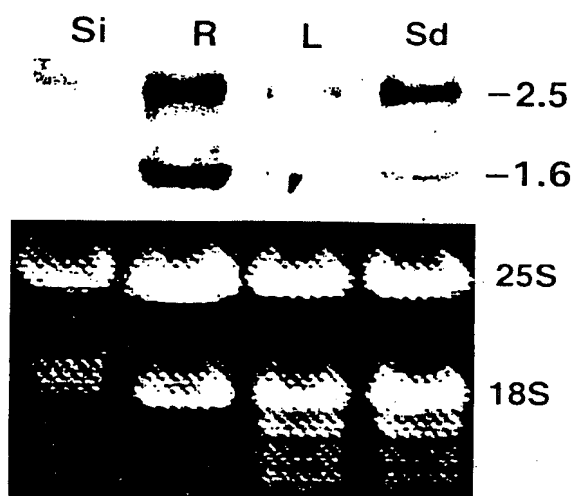


FIG.6A

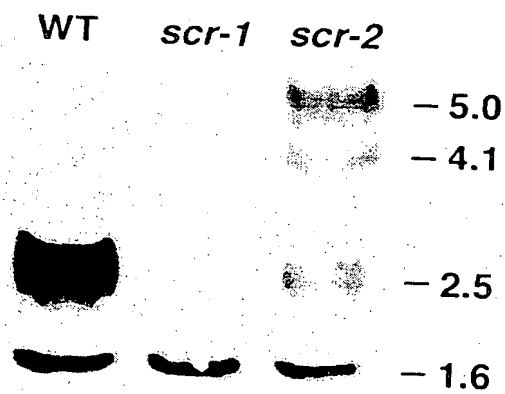


FIG.6B

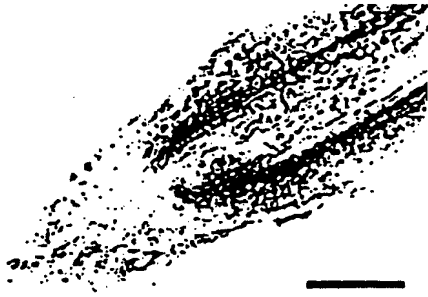


FIG.7A



FIG.7C



FIG.7B



FIG.7D

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FIG.7E

FIG.7F

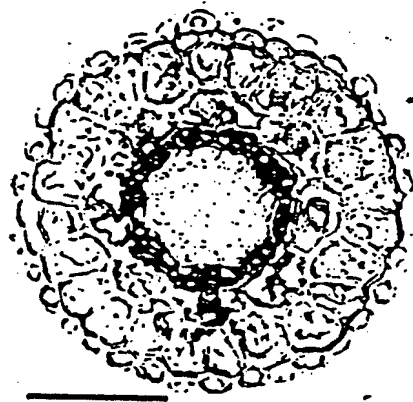
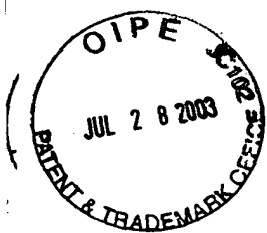


FIG.7G



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10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GGCACGAGCC	CAACGGGTCC	TGAGCTTCTT	ACTTATATGC	ATATCTTGTA	50
G T S P	T G P	E L L	T Y M H	I L Y	
TGAAGCCTGC	CCTTATTTCA	AATTCCGTTA	TGAATCTGCT	AATGGAGCTA	100
E A C	P Y F K	F G Y	E S A	N G A I	
TAGCTGAAGC	TGTGAAGAAC	GAAAGTTTTG	TGCACATTAT	CGATTTCAG	150
A E A	V K N	E S F V	H I I	D F Q	
ATTTCTCAAG	GTGGTCAATG	GGTGAGTTTG	ATCCGTGCTC	TTGGTGCTAG	200
I S Q G	G Q W	V S L	I R A L	G A R	
ACCTGGTGGA	CCTCCGAACG	TTAGGATAAC	GGGAATTGAT	GATCCGAGAT	250
P G G	P P N V	R I T	G I D	D P R S	
CATCGTTTGC	TCGTCAAGGA	GGACTTGAGT	TAGTTGGACA	AAGACTTGCG	300
S F A	R Q G	G L E L	V G Q	R L G	
AAGCTAGCTG	AAATGTGCGG	TGTTCCGTTT	GAGTCCATG	GAGCTGCTTT	350
K L A E	M C G	V P F	E F H G	A A L	
ATGCTGCACG	GAAGTCGAAA	TCGAGAAGCT	AGGAGTTAGA	AATGGAGAAG	400
C C T	E V E I	E K L	G V R	N G E A	
CGCTCGCGGT	TAACTTCCCG	CTTGTTCTTC	ACCACATGCC	TGATGAGAGT	450
L A V	N F P	L V L H	H M P	D E S	
GTAAGTGTGG	AGAATCACAG	AGATAGATTG	TTGAGATTGG	TCAAACACTT	500
V T V E	N H R	D R L	L R L V	K H L	
GTCACCAAAC	GTTGTGACTC	TGGTTGAGCA	AGAAGCGAAT	ACAAACACTG	550
S P N	V V T L	V E Q	E A N	T N T A	
CGCCGTTTCT	TCCCCGTTT	GTCGAGACAA	TGAACCATTA	CTTGGCAGIT	600
P F L	P R F	V E T M	N H Y	L A V	

FIG.8A



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10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TTCGAATCAA	TAGATGTGAA	ACTCGCTAGA	GATCACAAGG	AAAGGATCAA	650
F E S I	D V K	L A R	D H K E	R I N	
TGTTGAGCAG	CATTGTTTGG	CTAGAGAGGT	TGTGAATCTT	ATAGCTTGTG	700
V E Q	H C L A	R E V	V N L	I A C E	
AAGGTGTTGA	AAGAGAAGAG	AGGCACGAGC	CACTAGGGAA	ATGGAGGTCT	750
G V E	R E E	R H E P	L G K	W R S	
CGGTTTCACA	TGGCGGGATT	TAAACCGTAT	CCTTTGAGCT	CGTATGTGAA	800
R F H M	A G F	K P Y	P L S S	Y V N	
CGCAACAATC	AAAGGATTGC	TTGAGAGTTA	TTCAGAGAAG	TATACACTTG	850
A T I	K G L L	E S Y	S E K	Y T L E	
AAGAAAGAGA	TGGAGCATTG	TATTTAGGAT	GGAAGAATCA	ACCTCTTATC	900
E R D	G A L	Y L G W	K N Q	P L I	
ACTTCTTGTG	CTTGGAGGTA	ACTAATAAAA	ACCTTGTTGG	GTTTCAGAAG	950
T S C A	W R X				
AGATTAGAAA	CTTCTTTTAA	AGTTTGCAGA	ATCTGTTTGT	AAAAGTAAAA	1000
CTCATGCATG	ATCCGNAGGA	ACAAGTTGTC	AAATGTTGTA	GTAGTAAGTG	1050
ATATGTTGAT	GACCCAAAAA	AAAAAAAAAA	AAAAA		1085

FIG.8B



10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
GCTATGGAAG	GAGAGAAGAT	GGTTCATGTG	ATTGATCTCG	ATGCTTCTGA	50
A M E G	E K M	V H V	I D L D	A S E	
GCCAGCTCAA	TGGCTTGCTT	TGCTTCAAGC	TTTAACTCT	AGGCCTGAAG	100
P A Q	W L A L	L Q A	F N S	R P E G	
GTCCACCTCA	TTTGAGAATC	ACTGGTGTTC	ATCACCAGAA	GGAAGTGCTT	150
P P H	L R I	T G V H	H Q K	E V L	
GAACAAATGG	CTCATAGACT	CATTGAGGAA	GCAGAGAAAC	TCGATATCCC	200
E Q M A	H R L	I E E	A E K L	D I P	
GTTTCAGTTT	AATCCCGTTG	TGAGTAGGTT	AGACTGTTTA	AATGTAGAAC	250
F Q F	N P V V	S R L	D C L	N V E Q	
AGTTGCGGGT	TAAACAGGA	GAGGCCTTAG	CCGTTAGCTC	GGTTCCTCAA	300
L R V	K T G	E A L A	V S S	V L Q	
TTGCATACCT	TCTTGGCCTC	TGATGATGAT	CTCATGAGAA	AGAACTGCGC	350
L H T F	L A S	D D D	L M R K	N C A	
TTTACGGTTT	CAGAACAACC	CTAGTGGAGT	TGACTTGACAG	AGAGTTCTAA	400
L R F	Q N N P	S G V	D L Q	R V L M	
TGATGAGCCA	TGGCTCTGCA	GCTGAGGCAC	GTGAGAATGA	TATGAGTAAC	450
M S H	G S A	A E A R	E N D	M S N	
AACAATGGGT	ATAGCCCTAG	CGGTGAGTCG	GCCTCATCTT	TGCCTTTACC	500
N N G Y	S P S	G D S	A S S L	P L P	
AAGTTCAGGA	AGGACTGATA	GCTTCCTCAA	TGCTATTTGG	GGTTTGTCTC	550
S S G	R T D S	F L N	A I W	G L S P	
CAAAGGTCAT	GGTGGTCACT	GAGCAAGACT	CAGACCACAA	CGGCTCCACA	600
K V M	V V T	E Q D S	D H N	G S T	

FIG.9A



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10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CTAATGGAGA	GCCTATTAGA	ATCACTTTAC	ACCTACGCAG	CATTGTTTGA	650
L M E R	L L E S	L Y T Y	A A L F	D	
TTGCTTGGA	ACAAAAGTTC	CAAGAACGTC	TCAAGATAGG	ATCAAAGTGG	700
C L E	T K V P	R T S Q	D R I K	V E	
AGAAGATGCT	CTTCGGGGAG	GAGATCAAGA	ACATCATATC	CTCGGAGGGA	750
K M L	F G E E	I K N I	I S C E	G	
TTTGAGAGAA	GAGAAAGACA	CGAGAAGCTT	GAGAAATGGA	GCCAGAGGAT	800
F E R R	E R H E	K L E K	W S Q R	I	
DGATTTGGCT	GGTTTTGGGA	ATGTTCTCT	TAGCTATTAT	GCGATGTTGC	850
D L A	G F G N	V P L S	Y Y A M	L Q	
AGGCTAGGAG	ATTGCTTCAA	GGGTGCGGTT	TTGATGGGTA	TAGAATCAAG	900
A R R	L L Q G	C G F D	G Y R I	K	
GAAGAGACCG	GGTGCCAGT	AATTGCTGG	CAAGATCGAC	CTCTATACTC	950
E E S G	C A V I	C W Q D	R P L Y	S	
GGTATCAGCT	TGGAGATGCA	GGAAGTGAAT	GATATATTAC	AGTTTGTCTT	1000
V S A	W R C R	K X			
CTATTTTGGT	TATGAGCAGA	GTCCCTTTCT	TTTTTGATA	CATGGGGACA	1050
CAATCTTAGT	TGTTTTGTGA	TGGTGACTTT	CTGTCTCTTT	ATGCTATTTT	1100
GGCTTAAATG	CTTCTACTGC	CTCTGCATGT	AAAGCCTTTG	TGTGTTGGTT	1150
CAATTTGGTC	TGGTGTGGGT	GTAATACCAA	ACCAAATCCA	ATTGAGCTG	1200
AAGATAACTA	ATTGATGAT	CGGCTCGTGC	C		1231

FIG.9B

FIG. 10

CTTTGTCAAT GGTAATGAG CTGAGGCAGA TAGTTTCTAT CCAAGGAGAC 50
CCTTCTCAGA GAATCGCAGC TTACATGGTG GAAGGTCTAG CTGCAAGAAT 100
GGCCGCTTCA GGAAATTC A TCTACAGAGC ATTGAAATGC AAAGAGCCTC 150
CTTCGGATGA GAGGCTTGCA GCTATGCAAG TCCTGTTTGA AGTCTGCCCT 200
TGTTTCAAGT TCGGGTTTTT AGCAGCTAAT GGTGCGATAC TTGAAGCAAT 250
CAAAGGTGAA GAAGAAGTTC ACATAATCGA TTTCGATATA AACCAAGGA 300
ACCAATACAT GACACTGATA CGAAGCATTG CTGAGTTGCC TGGTAAACGA 350
CCTCGCCTGA GGTTAACAGG AATTGATGAC CCTGAATCAG TCCAACGCTC 400
CATTGGAGGG CTAAGAATCA TCAATCTAAG ACTCGAGCAA CTCGCAGAGG 450
ATAATGGAGT ATCCTTCAAA TTCAAAGCAA TGCCTTCAA GACTTCGATT 500
GTCTCTCCAT CAACACTCGG TTGCAAAACCA GGAGAAACCT TAATCAGTGA 550
ACTTTGCATT CCAACTTCAC CACATGCCCTG ACGAGAGTGT CACAACAGTA 600
AACCAGCGGG ACGAGCTACT TCACATGGTC AAAAGCTTAA ACCCGCTTGT 650
CACGGTCGTT GAACAAGACG TGAACACAAA CACTTCACCG TTCTTTCCCA 700
GATTCATAGA GGCTTACGAA TACTACTCAG CAGTTTTCGA GTCTCTAGAC 750
ATGACACTTC CAAGAGAAAG CCAAGAGAGG ATGAATGTAG AAAGACAGTG 800
TCTCGCTAGA GACATAGTCA ACATTGTTGC TTGCGAAGGA GAAGAACGGA 850
TAGAGAGATA CGAGGCTGGG GGAAATGGA GAGCAAGGAT GATGATGGCT 900
GGATTCAATC CAAAACCAAT GAGTGCTAAA GTAACCAACA ATATACAAA 950
CTGATAAAG CAACAATATT GCAATAAGTA CAAGCTTAAA GAAGAAATGG 1000
GTGAGCTCCA TTTTGTCTGG GAGGAGAAA GCTTAATCGT TGCTTCAGCT 1050
TGGAGGTAAG ATAAGTGACA AGAGCATATA GTCTTTATGT TTCATAAAC 1100
ATAATTATGT TTTTACTGTA ATCTTGGGTT ATTGTGTAC TGGTTAAATC 1150
ATCTCCATGT ATTATTACCA GAGGTTAGGG GTGATCACAG GTACTAAAAG 1200
CTAATCTAAC ACTTATGGAA GAATTTTTCT TTCTTTTTTT TCCCTATTAT 1250
ATAAAAATAA TTAGAGTTTT GTTCTTAAAC CTATTTGCTA AGTGTGAATG 1300
AGTCTTTACA TGTTCAATTT TCAGTTCAAA TGGTTAAATT TGTTAAGGTT 1350
CTCACTTAAA AAAAAA



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Zm-scl1

	10	20	30	40	50
	CCAGGAGGCGTTCGAGCGGGAGGAGCGTGTGCACATCATCGACCTCGACA				
	Q E A F E R E E R V H I I D L D I				
	60	70	80	90	100
	TCATGCAGGGGCTGCAGTGGCCGGGCCTCTTCCACATCCTTGCCCTCCCGC				
	M Q G L Q W P G L F H I L A S R				

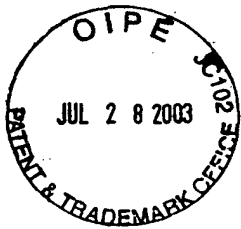
FIG.11A



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10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
CACGCGTCCG	TCAAAGGATA	CAACCATGTA	CACATAATTG	ACTTTTCCCT	50
H A S V	K G Y	N H V	H I I D	F S L	
GATGCAAGGT	CTCCAGTGGC	CGGCACTCAT	GGATGTCTTC	TCCGCCCCGTG	100
M Q G	L Q W P	A L M	D V F	S A R E	
AGGGTGGGCC	ACCAAAGCTC	CGAATCACAG	GCATTGGCCC	GAACCCAATA	150
G G P	P K L	R I T G	I G P	N P I	
GGTGGCCGTG	ACGAGCTCCA	TGAAGTGGGA	ATTCGCCTCG	CCAAGTATGC	200
G G R D	E L H	E V G	I R L A	K Y A	
ACACTCGGTG	GGTATCGACT	TCACTTTCCA	GGGAGTCTGT	GTCGATCAAC	250
H S V	G I D F	T F Q	G V C	V D Q L	
TTGATAGGTT	GTGCGACTGG	ATGCTTCTCA	AACCAATCAA	AGGAGAGGCA	300
D R L	C D W	M L L K	P I K	G E A	
GTTGCCATAA	ACTCCATCCT	ACAACTCCAT	CGCCTCCTCG	TTGACCCAGA	350
V A I N	S I L	Q L H	R L L V	D P D	
TGCAAACCCA	GTGGTGCCCG	CACCAATAGA	TATCCTCCTC	AAATTGGTCA	400
A N P	V V P A	P I D	I L L	K L V I	
TCAAGATAAA	CCCCATGATC	TTCACGGTGG	TTGAGCATGA	GGCAGATCAC	450
K I N	P M I	F T V V	E H E	A D H	
AACAGACCAC	CACTACTAGA	GAGGTTCACT	AATGCCCTCT	TCCACTATGC	500
N R P P	L L E	R F T	N A L F	H Y A	
GACCATGTTT	GACTCTTTGG	AGGCCATGCA	TCGTTGTACC	AGTGGTAGAG	550
T M F	D S L E	A M H	R C T	S G R D	
ACATCACCGA	CTCACTCACA	GAGGTGTACC	TTGAGGTGA	GATTTTTCAC	600
I T D	S L T	E V Y L	R G E	I F D	

FIG.11B1



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10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
ATTGTCTGCG	GCGAGGGCAG	TGCACGCACC	GAACGTCATG	AGTTGTTTGG	650
I V C G	E G S	A R T	E R H E	L F G	
TCACTGGAGG	GAGAGGCTCA	CCTATGCTGG	GCTAACTCAA	GTGTGGTTGG	700
H W R	E R L T	Y A G	L T Q	V W F D	
ACCCCGATGA	GGTTGACACG	CTAAAAGACC	AGTTGATCCA	TGTGACATCC	750
P D E	V D T	L K D Q	L I H	V T S	
TTATCTGGCT	CTGGGTTCAA	CATCCTAGTG	TGTGATGGCA	GCCTTGCACT	800
L S G S	G F N	I L V	C D G S	L A L	
AGCGTGGCAT	AATCGCCCGT	TATATGTGGC	AACAGCTTGG	TGTGTGACAG	850
A W H	N R P L	Y V A	T A W	C V T G	
GAGGAAATGC	TGCCAGTTCC	ATGTTGGCA	ACATCTGTAA	GGGTACAAAT	900
G N A	A S S	M V G N	I C K	G T N	
GATAGTAGAA	GAAAGGAAAA	CCGTAATGGA	CCCATGGAGT	AGCAGGAAGA	950
D S R R	K E N	R N G	P M E X		
ATAACCATGT	CATGAGCAAA	TCGATCAAGT	AATAAAATGC	ACTGATGACA	1000
TGCATGGTGA	TCTAAAGTTT	TTTTGCGTGA	ATGTGCAATG	ACGAATTGTT	1050
CAATTTGAAT	AACCTAATCA	TGAGACTCAA	AAAAAAAAAA	AAA	1093

FIG.11B2

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50
100
150
200
250
300
350
400
450
500
550
600

CCCAACTGG GAAGCCCTTC CTCCGCTCCG CCTCCTACCT CAAGGAGGCC
CTCCTCCTCG CACTCGCCGA CAGCCACCAT GGCTCCTCCG GCGTCACCTC
GCCGCTCGAC GTTGCCCTCA AGCTTGCAGC ATACAAAGTCT TTCTCTGACC
TGTCACCTGT GCTCCAGTTC ACTAACTTA CCGCAACAAG GCGCTTCTTG
ATGAGATTGG TGGCATGGCA ACTTCCTGCA TCCATGTCAT TGACTTTGAT
CTCGGTGTTG GTGGTCAGTG GGCTTCCTTC TTGCAGGAGC TTGCCCAACCG
CCGGGAGCT GGAGGTATGG CCTTGCCGTT GTTGAAGCTC ACGGCTTTCA
TGTCGACTGC TTCTCACCAT CCACTGGAGC TGCACCTTAC CCAGGATAAC
CTCTCTCAGT TTGCCGCAGA GCTCAGAATT CCTTTCGAAT TCAATGCCGT
CAGTCTTGAT GCATTCAATC CTGCGGAATC TATTTCTTCC TCTGGTGATG
AAGTTGTTGC TGTAGCCTC CCTGTTGGCT GCTCTGCTCG TGCACCAACCG
CTGCCAGCGA TTCTTCGGTT GGTGAACACAG CTTTGTCCCTA AGGTTGTCGT
GGCTATTGAT C

FIG.12A



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TTTTTTTTT TTTTTTTTTT TTTTTTTTTT TACAGAGCAA CAGCAGTATA 50
ATATTAAATC TGTACCAACAC AACCAATTGA TAGGTTAAAT TACCCTCTAG 100
TCTCTACTCA TAAGCAGTGT TTCCAATGAG ATGATCATGG CTAATTGAGC 150
AGAGCATGGC AACAAACCTAA AGCAACATCA TTAGCTATAG AGACTGACAC 200
CAATATTCCT AAATCCACTA GGCTAGCTAA TAAGCTGCAA CGAAAAGCAA 250
TATGAAGAGT TCAACAGCTC AAGACAACAA TTTCATTTGC AACATTTAAT 300
TGCAAGAATA AATGGACATT ACTGGAGTGG TCGATGCTTG CAAACGGTGG 350
TGGAACCTTG GTGGAGTGAA GCTTATGGCT GATCAGCACCC GCCAAGATGA 400
TATGGATACA AGCTCCCCAC GCTGCCAGTA GAGCGTAAGA GCAGCTCCGC 450
GTTTCTCCAC ATGGAATCCT CGGACCCTGCA CCCGCTTCAG GAGGCAGTCT 500
GC

FIG. 12B



SCR MAESGDFNGGQPPPHSPLRTTSSGSSSSNNRGPPPPPLVMVRKR----LASEMSS
TF1 MKRD---HHQFQGRLSNHGTSSSSSISKDK--MMVKKKEEDGGNMDELLAV----
TF4 MKRDHHHHHQ-----DKKTMM--NEEDDGNGM-DELLAV-----

|----- MOTIF I -----|
SCR NPDYNNSSRPPRRVSHLLDSNYNTVTPQQPPSLTAAATVSSQPNPPLSVCGFSG
TF1 -LGYKVRSSSEMAEVALKLEQLETMMSNAQEDGLSHLATDAAHYNPSELYS-----
TF4 -LGYKVRSSSEMADVAQKLEQLEVMMSNVQEDDLSQLATETVHYNPAELYT-----

SCR LPVFPSDRGGRNVMSVQPMQDSSSSASPTVWDAIIRDLIHS----STSVSIPQL
TF1 -----WLDNMLSELNPPPLPASSNGLDPVL
TF4 -----WLD SMLTDLNPP-----SSN-AEYDL

SCR IQNVRDIIFPCNPNLGALLEYRLRSLMLLDPSSSSDPSPQTFEPLYQISNNPSP
TF1 PSPEICGFPXSDYDLKVI PXNAIYQFPAIDSSSSNN--Q-----
TF4 -----KAI-P-----GDILNQF-AIDSASSN--Q-----

FIG.13A

SCR PQQQQQHQQQQQHKPPPPPIQQQERENSSDAPPQPETVTATVPAVQNTAEAE
TF1 -----NKRLKSCSSPDMSMTSTGTQIGGVIGTIVTTTTTTAAAES
TF4 -----GGGDTYTTNKRLKCSNGVVETTTATAES

----- MOTIF II (DIMERIZATION?) -----
SCR LREKKEIKRQKQDEEGLHLLTLLQCAEAVSADNLEEANKLLLEISQLSTPYG
1110 LSMVNELRQIVSIQG
TF1 -----TRSVILVDSQENGVRVLVHALMACAEAIQQNNLTAEALVKQIGCLAVSQA
TF4 -----TRHVVLVDSQENGVRVLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQI
3988 QLGGKPFLL

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-----|-----
SCR TSAQRVAAYFSEAMSARLLNSCLGIYAALPSRWMPQTHSLKMVSAFQVFNIGISP
4818 GTSPT-GPELLTYMHILYEACP
1110 DPSQRIAAVMVEGLAARMAASGKFYRAL-KCKEPPS--DERLAAMQVLFVFCP
TF1 GAMRKVATYFAEALARR-----IY-RL-SPPQNQIDHCLSDTLQMHFYETCP
TF4 GAMRQVATYFAEALARR-----IY-RL-SPSQSPIDHSLSDTLQMHFYETCP
3989 ----RSASYLKEALLALADSHHGSSGVT-SPLDVA----LKLAAYKSFSDLSP

FIG.13B



----- MOTIF III (VHIID) -----

SCR 4818 LVKFSHTANQAIQEAFAEK--EDSVHIIDLDMQGLQWPGLFHILASRPGGPP-----HVR
1110 YKFGYESANGATAEAVKN--ESFVHIIDFQISQGGQWVSLIRALGARPGGPP-----NVR
3935 CFKEGFLAANGAILEAIKG--EEEVHIIDFDINQGNQYMTLIRSI AELPGKRP-----RLR
TF1 AMEG--EKQVHVHVIDLDASEPAQWLALLQAFNSRPEGPP-----HLR
TF4 YLKFAHFTANQAILEAFEG--KKRVHVHVIDFSMNQGLQWPALMQALALREGGPP-----TFR
3989 YLKFAHFTANQAILEAFQG--KKRVHVHVIDFSMSQGLQWPALMQALALRPGGPP-----VFR
18310 VLQFTNFTANKALLDEIGGMATSCIHVHVIDENLGVGGQWASFLQELAHRRGAGGMALPLLK
Zm-Sc11 HASVKG--YNHVHIIDFSLMQGLQWPALMDVFSAREGGPP-----KLR
Zm-Sc12 QEAFER--EERVHIIDLDMQGLQWPGLFHILASR
Human FAG--CRRVHVVDFIGIKQGMQWPALLXDLAL
GRNGRTL--WLGECHIDLWPLQGLLSQGLQALCARPLGAP-----HVF--

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FIG. 13C

	--- ---	MOTIF	IV (DIMERIZATION)	MOTIF V
SCR	LTG LGTSMEA	LQATGKR	LSDFTDK	LGLPFEFCPLAEKVNDLTERLNV
4818	ITGIDDPRSSFARQGG	LELVGQR	LGKLAEM	CGVPFEFHGAALCCTEVEIEKLG
1110	LTGIDDPESVQRSIGG	LRIINLR	LEQLAED	NGVSFKFKAMPSKTSIVSPSTLGC
3935	ITG VHHQKEV	LEQMAHR	LIEEAEK	LDIPFQFNPPVSRDCLNVEQLRV
TF1	LTGIGPPAPDNSDH	LHEVGCK	LAQLAEA	IHVEFEYRGE VANSLAD LDASMLELRP
TF4	LTGIGPPAPDNFDY	LHEVGCK	LAHLAEA	IHVEFEYRGE VANTLAD LDASMLELRP
3989	LTAFMSTASHHPLE	LHLTQDN	LSQFAAE	LRIPFEFNAVSLDAFNPAESISSSGDE
18310	ITGIGPNPIGRDE	LHEVGIR	LAKYAHS	VGIDFTFQGVCDQLDRLCDWMLLKPI
Human	LPGLHTLS...	LGLQXRH	LLVHMMA	LSYSYGRXP...

SCR	RKREAAVHWLQHSLYDVTGSDAHTLWLL---	QRLAPK-----
4818	RNGEALAVNFPLVLHMPDESVTVENHR---	DRLLRL-----
1110	KPGETL VNFAFQLHMPDESVTVNQR---	DELLHM-----
3935	KTGEALAVSSVLQLHTFLASDDDLMRKNC-	ALRFQNNPSGVDLQRVLMMSHGS
TF1	SDTEAVAVNSVFELHKLLGRXGGIEKVLG-	-----
TF4	SEIESVAVNSVFELHKLLGRPGAIDKVLG-	-----
18310	K-GEAVAINSIQLHRLLVDPDANPVVPAPIDILLK---	
3989	WVAVSLPVGCSARAPPLPAILRLVKQLCPKVVAID	

FIG. 13D



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|-----
-----VTV-
-----VKHLSN-VVTL-
-----VKSLNPK-LVTV-
AAEARENDMSNNNGYSPSGDSASSLPLPSSGRDTSFLNAINGLSPKVMVVT-
-----VVKQD*TGDFHXW
-----VWNQIKPEIFTV-
-----LVIKINPMIFTV-

SCR
4818
1110
3935
TF1
TF4
18310

----- MOTIF VI -----
VEQDLSHAGS--FLG-RFVEAIHYYSALFDSLGSYGEESE---ERHVVEQQ
VEQEANTNTAP-FLP-RFVETMNHYLAVFESIDVKLARDHK---ERINVEQH
VEQDVNTNTSP-FFP-RFIEAYEYYSAVFESLDMTLPRESQ---ERMNVERQ
-EQDSDHNGS--TLMERLLESLYTYAALFDCLETKVPRTSQ---DRIKVEKM
XRQEPNHNG-PGFLD-GXTESLHYSTXFDLSLEG--XPNSQ---DKLMSEXY
VEQESNHNS-PIFLD-RFTESLHYSTLFDSLEG--VPSGQ---DKVMSEVY
VEHEADHNR-PPLLE-RFTNALFHYATMFDLSLEAMHTCTSGRDTDSLTEVY

SCR
4818
1110
3935
TF1
TF4
18310

FIG.13E



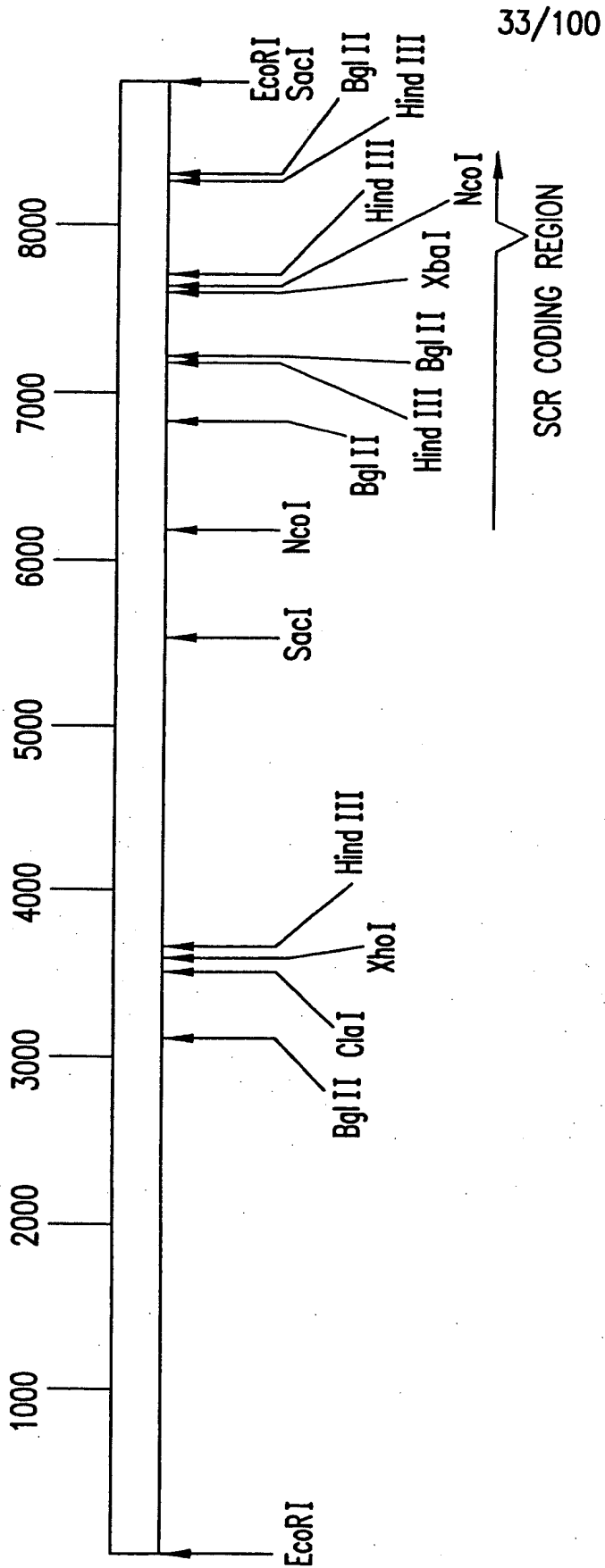
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SCR LLSKEIRNVLA VGGPSRSGEVKFE-SWREKMQCGFKGIS-
4818 CLAREVUNLIACEGVEREERHEPLGKWSRFHMAFGKPY-
1110 CLARDIVNIVACEGEERIEREYEAAGKWRARMMAGFNP-
3935 LFGEEIKNIIISCEGFERRERHEKLEKWSQRIDLAGEGNVP-
TF1 -LGXQICNLVACEGPPDRVERHETLSQWGNRFGSSGLAPAH-
TF4 -LGKQICNVVACDGPDRVERHETLSQWRNRFSGSAGFAAAH-
18310 -LRGEIFDIVCGEGSARTERHELFGHWRERLTYAGLTQVWF

-----|
SCR LAGNAATQATLLGMFPS-DGYTLVDDN-GTLKLGWKDLSLLTASAWTPRS*
4818 LSSYVNATIKGLLES-YS-EKYTL-EERDGAlyLGWKNQPLITSCAWR*
1110 MSAKVNTNIIQNLIKQCYC-NKYKLKEEM-GELHFCWEEKSLIVASAWR*
3935 LSYYAMLQARRLLQCGGF-DGYRIKEES-GCAVICWQDRPLYSVSAWRCRK*
TF1 LGSNAFKQASMLLSVFNNSGQGYRV-EESNGCLMLGWHTRPLITTSAWKLSTAAH*
TF4 IGSNAFKQASMLLALFNNGGEGYRV-EESDGCCLMLGWHTRPLIATS AWKLSTN*
3989 ADCLL-KRVQVRGFHV-EKRGAAALTYWQRGELVSISSWRC*
18310 DPDEVDTLKDQLIHVTSLSGSGFNILVCDGSLALAWHNRPLYVATAWCVTGNA

FIG. 13F

18310 SSMVGNICKGTNDSRRKENRNGPME*



SacI GENOMIC FRAGMENT

HIII-SacI CLONE

FIG.14

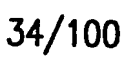


FIG. 15A



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```

Scr
3989
12398
4871
11846
2504
3935
11261
713
10964
23196
Tf1
Tf4
18310
18652
4818
21729
1110
174
33/08

```

FIG. 15B



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```

SCR
3989
12398
4871
11846
2504
3935
11261
713
10964
23196
Tf1
Tf4
18310
18652
4818
21729
1110
174
33/08

```

FIG. 15C



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SCR	MAESGDFNGG	QPPPHSPLRT	TSSGSSSSNN	RGPPPPPPPP	LVMVRKRLAS
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	CMFHDALALQ	AAEKSLYEAL	GEKDPSSSSA	SSVDHPERLA	SHSPDGSCSG
Tf1
Tf4
18310
18652
4818
21729
1110
174
33/08TSDSA	SSFNIPTSAQ	NHYATGSFST
					50
					1

FIG.15D

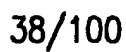


FIG. 15E



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SCR	LSVCGFSGLP	VFPSDRGGRN	VMMSVQPMQ	DSSSSASPT	VWVDIIRDL
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	TGGGGGNSA	VYGSFGDDL	VSNMFKDDEL	AMQFKKGVEE	ASKFLPKSSQ
Tf1	GNMDELLAV	LGYKVRSEM	AEVALKLEQL	ETMMSNAQED	GLSHLATDAA
Tf4	NGM.DELLAV	LGYKVRSEM	ADVAQKLEQL	EVMMSNVQED	DLSQLATETV
18310
18652
4818
21729D
1110
174
	101				150

FIG. 15F



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SCR	IHSSTSVSIP	QLIQNVVDII	FPCNPNLGAL	LEYRLRSLML	LDPSSSSDPS
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	LFIDVDSYIP	MNSGSKENG	EVFVKTEKCD	ETEHHHHSY	APPPNRLTGK
Tf1	HYNPSELYSW	LDNMLSELNP	PPLPASSNGL	DPVLPSEIC	GFPXSDYDLK
Tf4	HYNPAELYTW	LDSMLTDLNP	P.....SSNA.EYDLK
18310
18652
4818
21729	LTSVNDMSLF	GGSGSSQRYG	LPVPRSQTQQ	QQSDYGLFGG	IRMGIGSGIN
1110
174
151
					200

FIG.15G



SCR	PQTFFELYQI	SNNPSPPOQQ	QQHQQQQQQH	KPPPPPIQQQ	ERENSSTDAP
3989
12398
4871
11846
2504
3935
11261
713
10964
23196	KSHWRDEDED	VEERSNKQSA	VYVEEELSE	MFDNMFLCGP	GKPVICILNQ
Tf1	VIPXNAIYQF	PAIDSSSSN	NQ.....	NKRLKSCSSP	DSMVTSTSTG
Tf4	AIPGDAILNQ	FAIDSASSN	QGGGDTYTT	NKRLKCS
18310
18652
4818
21729	NYPTLTGVPC	IEPVQNRVHE	SENMLNSLRE	LEKQLLDDDD	ESGGDDDDSV
1110
174
	201				250

FIG. 15H



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```

|<--- bZIP like domain --->|
|<--- Motif II (dimerization)|
Scr  PQPETVTATV PAVQNTAEALRRKEEIKR QKQDEEGLHL LTLLLQCAEA
3989  .....
12398 .....
4871  .....AAIFYG HHHHTPPPAK RLNPGPVGIT
11846 .....
2504  .....
3935  .....
11261 .....
713   .....
10964 .....
23196 NFPTESAKVV TAQSNQAKIR GKKSTSTSHS NDSKKETADL RTLLVLCAQA
Tf1  TQIGGVIGTT VTTTTTTTA AAESTRSVIL VDSQENGVRV VHALMACAEA
Tf4  ...NGVVE...TTTA TAESTRHHVVL VDSQENGVRV VHALMACAEA
18310 .....
18652 .....
4818  .....
21729 ITNSNSDWIQ NLVTPNPNN PVLSPSPSS SSSSSPSTAS TTTSVCSRQT
1110  .....
174   .....
251   .....
300   .....

```

FIG.15I

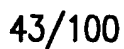


FIG. 15J



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←-- Motif III (SCR VHIID) ---
AALPSRWMPQ THSLKMVSFAF QVENGISPLV KFSHFTANQA IQEAFEKEDS
3989 LYNKALL DEIGGMATSC
12398
4871 LHNVSQTLA CSLIFKVAAY KSFSEISPLV QFANFTSNQA LLESFHGFHR
11846
2504
3935 AMEGEKM
11261
713
10964
23196 TALS...SKK TSAADMLKAY QTYMSVCPFK KAAIIFANHS MMRFTANANT
Tf1 QIDHCLSDT.LQ MHFYETCPYL KFAHFTANQA ILEAFEGKKR
Tf4 PIDHSLSDT.LQ MHFYETCPYL KFAHFTANQA ILEAFQGKKR
18310 HA SVKGYN...H
18652 ANVE ILEAIAGETR
4818 SPTGPELLT.YM HILYEACPYF KFGYESANGA IAEAVKNESF
21729 SPVTELYGKE HLISTQL... ..LYELSPCF KLGFEAAANLA ILDAADNNDGMMI
1110 EPPSDERLA.AM QVLFEVCPCF KFGFLAANGA ILEAIKGEET
174
351 400

FIG.15K

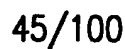


FIG. 15L

	← --- Motif V ---	
	--- Motif IV ---	
Scr	ATGKRLSDFT DKLGPFEEFC PLAELKVGNDL TERLNVKRE AVAVHWL...	
3989	LHLTQDNLSQ FAEELRIPFE FNAVSLDAFN PAESISSGD EVVAVSL...	
12398	
4871	FTQDNLKHFA SEINISLDIQ VL..SLDLG SISWPNSS.. EKEAVAVNIS	
11846	
2504NGGAF APSTWTA...	
3935	QMAHRLIEEA EKLDIPFQFN PVSRLDCLN VE...QLRVK TGEALAVSSV	
11261K KWETITLDEL MINPGETTVV	
713	
10964	
23196	EFRQVIAWL DTVSDTMFRL STQQLRNGE TIQVEDLKLQ QGEYVVVNSL	
Tf1	EVGCKLAQLA EAIHVEFEYR GFVANSLADL DASMLELRPS DTEAVAVNSV	
Tf4	EVGCKLAHLA EAIHVEFEYR GFVANTLADL DASMLELRPS EIESVAVNSV	
18310	EVGIRLAKYA HSVGIDFTFQ GVCVDQLDRL CDWML.LKPI KGEAVAINSI	
18652	LVGERLATLA QSCGVPEFEH D...AIMSGC KVQREHLGLE PGFAVVVNFP	
4818	LVGQRLGKLA EMCGVPPEFH G...AALFCT EVEIEKLGVR NGEALAVNFP	
21729	AVGDLLSQLG DHSISVSFNV V...TSLRLG DLNRESLGCD PDETAVNLA	
1110	IIGLRLEQLA EDNGVSFKFK A...MPSKTS IVSPSTLGCK PGETLIVNFA	
174	
	451	500

FIG.15M



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	Motif V	
SCR	QHS	...
3989	P VG	...
12398		...
4871	AA	...
11846		...
2504	R SL	...
3935	LQLHTFLASD DDLMRKNCAL REHNPSGVD LQRLVLMMSGH SAAEAARENDM	...
11261	NCIHRQLQYTP DE	...
713		...
10964		...
23196	FRFRNLL... DE	...
Tf1	FELHKLLGRX GG	...
Tf4	FELHKLLGRP GA	...
18310	LQLHRLLVDP DA	...
18652	YVLHHM... P DE	...
4818	LVLHHM... P DE	...
21729	FKLYRV... P DE	...
1110	FQLHHM... P DE	...
174		...
		501
		550

FIG.15N



	Motif V ----->		<--- Motif VI ---
Scr	LYDVTGSD	AHTLWLLQRL
3989	APKVVTVVEQ
12398	CSARAPPL	PAILRLVKQL
4871	CPKVVVAIDH
11846	GGDRADLPFS
2504	SFSLPLV
3935	WTARSLPVPSSPST	RTDLPFSQQL
11261	DSASSLPSPSSGRT
713	TVSLDSPR	EADHNKTGFL
10964
23196
Tf1
Tf4
18310
18652
4818
21729
1110
174
551
			600

FIG.150



----- Motif VI -----
SC1 GRFVEAIHYY SALFDSLGLAS Y..GEESEER HVVEQQLLSK EIRNVLA VGG
3989 QHFLNCFQSC VFLDSLDAAG I..DADSA.. CKIERFLIQP RVEDAVIG..
12398 SLEPN L..DRDSKER LRVERVLFG RIMDLVRSDD
4871 AHSLHSHTAL FESLDAVNAN L..DAM.... QKIERFLIQP EIEKLVLD..
11846 DRFTEALFY SAVFDSLDA A N..NNNNNN QRMEA EYLQR EICDIVCGEG
2504
3935 ERLLESLYTY AALFDCLETK V..PRTSODR IKVEKMLFGE EIKNIISCEG
11261 TRFREALFHY SSLFDMFDTT IHADEYKNR SLLERELLVR DAMRVISCEG
713 TRFREALFHY SAIFDMLETN I..PKDNEQR LLIESALFSR E.XNVISCEG
10964 TRFREALFHF SSIFDMLETI V..PREDEER MFLEMEVFGR EALNVIACEG
23196 TRFREALFHY SAVFDMCD SK L..AREDEMR LMVVF EFGYGR EIVNVVASEG
Tf1 DGXTESLHYY STXFDSLEGX ...PNSQD.. KLMSEXYLGX QICNLVACEG
Tf4 DRFTESLHYY STLFDSLEGV ...PSGQD.. KVMSEVYLGK QICNVVACDG
18310 ERFETNALFHY ATMFDSLEAM HRCTSGRDIT DSLTEVYLRG EIFDIVCGEG
18652 SRFVETLDYY TAMFESIDAA R..PRDDKQR ISAEQHCVAR DIVNMIACEE
4818 PRFVETMNHY LAVFESIDVK L..ARDHKE R INVEQHCLAR EVENLIACEG
21729 GRVSESCACY GALLESVES T V..PSTNSDR AKVE.EGIGR KLVNAVACEG
1110 PRFIEAYEYY SAVFESLDM T L..PRESQER MNVERQCLAR DIVNIVACEG
174RXFDSLEHD A..SKGEPRE DERGRXCLAR NIVNIVXCKX
601 650

FIG.15P



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Scr	PSRSGEVKF.ESWRE	KMQCGFKGI	SLAG..NAAT	QATLLGMFP
3989	.RHKA..Q..	...KAIAWRS	VFAATGKPV	QLSN..LAEA	QADCLLKRVQ
12398	DNNKPGTRFG	LMEEKEQWRV	LMEKAGFEPV	KPSN..YAVS	QAKLLWNYN
4871	.RSRPIER..	...PMMTWQA	MFLQMGFSPV	THSN..FTES	QAECLVQRTF
11846	AARXERHE..	...PLSRWRD	RLTRAGLSAV	PLG.....SNA
2504
3935	FERRERHE..	...KLEKWSQ	RIDLAGFNV	PLSY..YAML	QARRLLQCGG
11261	AERFARPE..	...TYKQWRV	RILRAGFKPA	TIS....KQI	MKEAKEIVRK
713	LERMERPE..	...TYKQWQV	RNQRVGFQQL	PLN....QDM	MKRARXEGQV
10964	WERVERPE..	...TYKQWHV	RAMRSGLVQV	PFD....PSI	MKTSLHKVHT
23196	TERVESRE..	...TYKQWQA	RLIRAGFRQL	PLE....KEL	MONLKLKIEN
Tf1	PDRVERHE..	...TLSQWGN	RFGSSGLAPA	HLGS...NAF	KQASMLLSVF
Tf4	PDRVERHE..	...TLSQWRN	RFGSAGFAAA	HIGS...NAF	KQASMLLALF
18310	SARTERHE..	...LFGHWR	RLTYAGLTQV	WFDPEVDTL	KDQLIHVTSL
18652	SERVERHE..	...VLGKWRV	RMMAGFTGW	PVSTSAAF	SE....MLK.
4818	VEREERHE..	...PLGKWR	RFHMAGFKPY	PLSSYVNATI	KG....LLE.
21729	IDRIERCE..	...VFGKWRM	RMSMAGFELM	PLSEKIAESM	KS....RGNR
1110	EERIERYE..	...AAGKWRA	RMMAGFNP	PMSAKVTNNI	QN....LIKQ
174	EERIERYE..	...VTGKWRA	RMMAGFSR	PMSGRVTSNI	ES....LIK
	651				700

FIG.15Q



----- Motif VI ----->

SCR	.SDGYTLVD.	DNGTLKLGWK	DLSLLTASAW	TPRSX
3989	VRGFH..VEK	RGAAALTLYWQ	RGELVSISW	RCX
12398	YSTLYSLVES	EPGFISLAWN	NVPLLTVSSW	RX
4871	VRGFH..VEE	KHNSLLLCWQ	RTELVGVSAW	RCRSSX
11846
2504
3935	FDGYR..IKE	ESGCAVICWQ	DRPLYSVSAW	RCRKX
11261	RYHRDFVIDS	DNNWMLQGK	GRVIYAFSCW	KPAEKFTNNN	LNIX
713	LPTRTFIIDE	DNRWLLQGK	GRILFALSTW	KPDNRSSX
10964	FYHKDFVIDQ	DNRWLLQGK	GRTVMALSVW	KPESX
23196	GYDKNFDVDQ	NGNWLLQGK	GRIVYASSLW	VPSSX
Tf1	NSGQGYRVEE	SNGCLMLGWH	TRPLITTSAW	KLSTAAHX
Tf4	NGGEGYRVEE	SDGCLMLGWH	TRPLIATSAW	KLSTNX
18310	.SGSGFNILV	CDGSLALAWH	NRPLYVATAW	CVTGGNAASS	MVGNICCKGTN
18652	AYDKNYKLG	HEGALYLFWK	RRPMATCSVW	KPNPNYIGX
4818	SYSEKYTLEE	RDGALYLGWK	NQPLITSCAW	RX
21729	VHPG.FTVKE	DNGGVCFGWM	GRALTVASAW	RX
1110	QYCNKYKLKE	EMGELHFCWE	EKSLIVASAW	RX
174	DYCSKYKVKE	EMGELHFSWE	EKSLIVASAW	SX
					750
					701

FIG.15R



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Scf
3989
12398
4871
11846
2504
3935
11261
713
10964
23196
Tf1
Tf4
18310	DSRRKENRNG	PMEX
18652
4818
21729
1110
174
	751	764

FIG. 15S



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SRPa1 (1110)

CTTTGTCAATGGTAAATGAGCTGAGGCAGATAGTTTCTATCCAAGGAGACCCCTTCTCAGA
GAATCGCAGCTTACATGGTGAAGGTCTAGCTGCAAGAATGGCCGCTTCAGGAAATTCATCA
TCTACAGAGCATTTGAAATGCAAGAGCCCTCCTTCGGATGAGAGGCTTGCGAGCTATGCAAG
TCCTGTTTGAAGTCTGCCCTTGTTCAGTTTCGGGTTTTCAGCAGCTAATGGTCCGATAC
TTGAAGCAATCAAGGTGAAGAAGATTACATAATCGATTTCGATATAAACCAGGGA
ACCAATACATGACACTGATACGAAGCATTCGTGAGTTGCCCTGGTAACGACCTCGCCTGA
GGTTAACAGGAATTGATGACCCCTGAATCAGTCCAAACGCTCCATTGGAGGGCTAAGAAATCA
TCGGTCTAAGACTCGAGCAACTCGCAGAGGATAATGGAGTATCCTTCAAATTCAAAGCAA
TGCCTTCAAAGACTTCGATTGTCTCTCCATCAACAACCTCGTTGCAACACGAGGAAACCT
TAATAGTGAACCTTTGCATTCCAACTTCACCACATGCCCTGACGAGAGTGTCAACACAGTAA
ACCAGCGGACGAGCTACTTCACATGGTCAAAAGCTTAAACCCAAAGCTTGTACGGTACG
TTGAACAAGACGTGAACACAAACACTTCACCGTTCTTTCCAGATTTCATAGAGGCTTACG
AATACTACTCAGCAGTTTTCGAGTCTCTAGACATGACACTTCCAAGAGAAAGCCAAAGAGA
GGATGAATGTAGAAAGACAGTGTCTCGCTAGAGACATAGTCAACATTTGCTTGCGAAG
GAGAAGAACGGATAGAGAGATACGAGGCTCGGGGAAATAATGGAGAGCAAGGATGATGAG
CTGGATTCAATCCAAAACCAATGAGTGCTAAAGTAACCAACAATATACAAAACCTGATAA
AGCAACAATATTGCAATAAGTACAAGCTTAAAGAGAAATGGGTGAGCTCCATTTTGTGCT
GGGAGGAGAAAAGCTTAATCGTTGCTTCAGCTTGAGGTAAGATAAGTGACAAGAGCATA
TAGTCTTTATGTTTCATAAAACATAAATTATGTTTTTACTGTAATCTTGGGTTATTGTGTA
ACTGGTTAAATCATCTCCATGTATTATTACCAGAGGTTAGGGGTGATCACAGGTACTAAA
AGCTAATCTAACACTTATGGAAGAAATTTTCTTTTCTTTTTCCTTATATATAAAAT
AATTAGAGTTTTCGTTCTAAACCTATTTCGCTAAGTGTGAATGAGTCTTTTACATGTTTCATA
TTTCAGTTCAAATGGTTAAATTGTTAAGGTTCTCACTTAAAAAAAA

FIG. 16A



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SRPa3 (3935)

GCTATGGAAGGAGAGAAGATGGTTCAATGTGATTGATCTCGATGCTTCTGAGCCAGCTCAA
TGGCTTGCTTTGCTTCAAGCTTTTAACTCTAGGCTGAAGTCCACCTCATTTGAGAAATC
ACTGGTGTTCATCACCAGAAGGAGTGCTTGAACAAATGGCTCATAGACTCATTTGAGGAA
GCAGAGAAACTCGATATCCCGTTTCAGTTTAAATCCCGTTGTGAGTAGGTTAGACTGTTTA
AATGTAGAAACAGTTGCGGTTAAACACAGGAGAGGCCCTTAGCCGTTAGCTCGGTTCTTCAA
TTGCATACCTTCTTGCCCTCTGATGATGATCTCATGAGAAAGAACTGCGCTTTACGGTTT
CAGAACACCCCTAGTGGAGTTGACTTGCAGAGAGTTCTAATGATGAGCCATGGCTCTGCA
GCTGAGGCACGTGAGAAATGATATGAGTAAACAAATGGGTATAGCCCTAGCGGTGACTCG
GCCTCATCTTTGCCCTTACCAAGTTCAAGGAGGACTGATAGCTTCTCCTCAATGCTATTTGG
GGTTTGTCTCCAAGGTCATGGTGTCACTGAGCAAGACTCAGACCACAAACGGCTCCACA
CTAATGGAGAGGCTATTAGAAATCACTTACACCTACGCAGCATTTGTTGATTGCTTGGAA
ACAAAAGTTCCAAGAACGTCCTCAAGATAGGATCAAAAGTGGAGAAAGATGCTCTTCGGGGAG
GAGATCAAGAACATCATATCCTGCGAGGGATTGAGAGAGAGAGAAAGACACGAGAAAGCTT
GAGAAATGGAGCCAGAGGATCGATTGGCTGGTTTGGGAATGTTCCCTCTTAGCTATTAT
GCGATGTTGCAGGCTAGGAGATTGCTTCAAGGTTGCGGTTTGTGATGGGTATAGAAATCAAG
GAAGAGAGCGGGTGGCAGTAATTTGCTGGCAAGATCGACCTCTATACCTCGGTATCAGCT
TGGAGATGCAGGAAGTGAATGATATATACAGTTTGTCTTCTATTTTGGTTATGAGCAGA
GTCCCTTCTTTTGTATACATGGGGACACAAATCTTAGTTGTTTGTGATGGTGACTTT
CTGTCTCTTTATGCTATTTTGGCTTAAATGCTTCTACTGCCCTCTGCATGTAAAGCCCTTG
TGTGTTGGTTCAATTTGGTCTGGTGTGGGTGTAATACCAAACCAAAATCCAAATTTGAGCTG
AAGATAACTAATTTGATGATCGGCTCGTGCC

FIG. 16B

SRPa4 (4818)

GGCAGAGCCCAACGGGTCCTGAGCTTCTTACTTATATGCATATCTTGTATGAAGCCTGC
CCTTATTTCAAATTTCGGTTATGAATCTGCTAATGGAGCTATAGCTGAAGCTGTGAAGAAC
GAAAGTTTGTGCACATTATCGATTTCAGATTTCCTCAAGGTGGTCAATGGGTGAGTTTG
ATCCGTGCTCTTGGTGCTAGACCTGGTGACCTCCGAACCTTAGGATAACCGGAATTGAT
GATCCGAGATCATCGTTTGTCTCGTCAAGGAGGACTTGAGTTAGTTGGACAAAGACTTTGGG
AAGCTAGCTGAATGTGCGGTGTTCCGTTTGAGTTCATGGAGCTGCTTTATGCTGCACG
GAAGTCGAAATCGAGAAGCTAGGAGTTAGAAATGGAGAAGCGCTCGCGTTAACTTCCCG
CTTGTCTTCACCAATGCTGATGAGAGTGTAACCTGTGGAGAATCACAGAGATAGATTG
TTGAGATTGGTCAAAACACTTGTCAACCAACGTTGTGACTCTGGTTGAGCAAGAGCGAAT
ACAAACACTGCGCGGTTTCTTCCCGGTTTGTCTGAGACATGAACCATTAATTGGCAGTT
TTCGAATCAATAGATGTGAACCTCGCTAGAGATCACAGGAAGGATCAATGTTGAGCAG
CATTGTTTGGCTAGAGAGGTTGTGAATCTTATAGCTTGTGAAGGTGTTGAAGAGAGAAGAG
AGGCAGGCCACTAGGGAATGGAGGTCTCGGTTTCAATGGCGGGATTTAAACCGTAT
CCTTTGAGCTCGTATGTGAACGCAACATCAAGGATTGCTTGAGAGTTATTTCAGAGAAG
TATACACTTGAAGAAAGAGATGGAGCATTTGATTTAGGATGGAAGAAATCAACCTCTTATC
ACTTCTTGTGCTTGGAGGTAACTAATAAAACCTTGTTCGGTTTCAGAAAGAGATTAGAAA
CTTCTTTTAAAGTTTGCAGAAATCTGTTTGTAAAGTAAACTCATGATGATCCGNAGGA
ACAAGTTGTCAAATGTTGTAGTAGTAAGTGATATGTTGATGACCCCAAAAAA
AAAAA

FIG. 16C



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SRPa5 (4871)

GGGGCTATCTTCTACGGCCACCAACCACCATACACCTCCGCCGGCAAGCGGCTCAACCCCT
GGTCCCGTGGGATAACAGAGCAGCTGGTTAAGCAGCAGAGGTCAATAGAGCGACACG
TGCTAGCTCAGGGGATATTGGCGGGCTCAATCAACAGCTCTCTTCTCCCGTCGGGAAG
CCATTAGAAAGAGCAGCTTTTACTTCAAGAAGCTCTCAATAATCTCCTTCACAACGTC
TCCCAAACCCCTAAACCCCTTATTCCTCATCTTCAAGATCGCTGCTTACAAATCCTTCTCA
GAGATCTCTCCGTTCTTCAGTTCGCCAACTTTACCTCCAACCAAGCCCTCTTAGAGTCC
TTCCATGGCTTCCACCGTCTCCACATCATCGACTTCGATATCGGCTACGGTGGCCAAATGG
GCTTCCCTCATGCAAGAGCTTGTTCTCCGCGACAAACGCCGCTCCTCTCCTCAAGATC
ACCGTTTTCGGCTTCTCCGGCGAAACCAAGCCAGCTCGAACTTGGCTTCACTCAAGACAAC
CTCAAGCACTTCGCCCTCTGAGATCAACATCTCCCTTGACATCCAAATTTTGAGCTTAGAC
CTCCTCGGCTCCATCTCGTGGCCCTAACTCGTCGGAGAAAGAGCTGTCGCCGTTAACATC
TCCGCCCGCTCCTTCTCGCACCTCCCTTTGGTCTCCTCGTTTCGTGAAGCATCTATCTCCG
ACGATCATCGTCTGCTCCGACAGAGGATCGAGAGGACGGATCTGCCCTTCTCTCAACAG
CTCGCCCACTCGCTGCACTCACACACCGCTCTCTTTCGAATCCCTCGACGCCGTCAAGCC
AACCTCGACGCAATGCAGAAAGATCGAGAGGTTTCTTATACAGCCGGAGATAGAGAAGCTG
GTGTTGGATCGTAGCCGTCCGATAGAAAGCCGATGATGACGTGGCAAGCGATGTTTCTA
CAGATGGGTTTCTACCGGTGACGCACAGTAACCTCACGGAGTCTCAAGCCGAGTGTTTA
GTCCAAACGGACGCCAGTGAGAGGCTTTCAGTCGAGAAAGAAACATAACTCACTTCTCCTA
TGTTGGCAAGGACAGAACTCGTCGGAGTTTCAGCATGGAGATGTCGCTCCTCCTGATTT
CCACCGAGTTTCAATTATTAATAAAATATTTTCCTTAATTCAATTATCTTAATGACA
AATTTTGTAGTTTCTGATTTTATTTTGCTCAGTGGCATGATTTTAAATTTAAGTTTCAC
ACAAATATATAAATTTTGTG

FIG. 16D



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SRPa6 (12398)

AATCGCTGAACCGAATTGGATCGAGATTCGAAAGAAAGGCTGAGAGTGAGAGAGTGC
TGTTCCGCTAGGAGGATTATGGATTGGTCCGATCAGATGATGATAATAAACC GGAA
CCCCGTTGGGTTAATGGAGGAGAAAGAAACAATGGAGAGTGTGATGGAGAAAGCTGGAT
TTGAGCCGGTTAAACCGAGTAATTACGCGGTTAGCCAAAGCGAGCTGCTACTATGGAAC
ACAATTATAGTACATTGTATTCACTTGTGAATCGGAGCCAGGTTTCATCCTCGGCTT
GGAACAATGTGCTCTCCTCCTCACCGTTTCCCTCTGGCGTTGACTACTTGGTCCGATAAGTT
AATCTAGTATTTTGAGTTAGCTTTTAGAATTGAATTGTTGGGTTAGATTGGATGTTT
AATTAGTCTCTAGCCATTCTCTTACTCTTTTGTCTAGTGCTTGGAGTGATGATGGTT
TGTCGTTTATGTTTCATTGTAAATATATATTGTATGTAAACATTGACTAAAAA
AAAAAAA

FIG. 16E



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FIG. 16F-1

SRPa7 (21729/3635/17410)

AAAGACTTTAGCAGATTTTCAAGCGGCTCAGAACAATCAACAACAACAACAACAACCG
TTTTATAGTCAAGCAGCTCTCAACGCTTTTCTTTCAAGTCTGTGAAGCCTCGAAATTAT
CAGAAATTTCAATCTCCGTCGGCCGATGATGATCTCACGTCGGTGAATGATATGAGTTT
GTTTGGTGGTCTGTTTCATCTCAGCGTTACCGTTTACCGGTTCCAGGTCCTCAGACGCA
ACAGCAACAATCGGATTACGGTTTATTTGGTGGATCCGAATGGGAATCGGGTCGGGTAT
TAATAATTATCCAACATTAAACCGGCTTCCGTGTTATGAACCGGTTCAAAACCGGTTCA
TGAATCGGAGAACATGTTGAATAGTTTAAGAGAGCTTGAGAAACAGCTTTTAGATGATGA
CGATGAGAGTGGTGTGATGATGACGTGTGAGTTATAACAATAATCAAAATCCGATTGGAT
TCAAAATCTCGTGACTCCGAACCCGAACCCGGTTTGTCTTTTTCACCGAGCTC
TTCCTTCTCGTCTTCTTCGCTTCTACAGCTTCGACGACGACATCGGTATGTTCTAGGCA
AACGGTTATGGAATCGGACGGCGATCGCGAAGGAAACAGAGATAGCGACGGAGAT
TTTGGCGCGTGTCTCAACCGCCTAATCTTGAGAGGAATTCAGAGCAGAAAGCTTGTGA
TTTCATGTGGTGGCTTCGATCGAGGATAGCTTCTCCAGTGACGGAATTGTATGGGA
GGAGCATTTAATCTCGACTCAATTGCTCTACGAGCTCTCTCTGTTTCAAACTCGGTTT
CGAGCGCGGAATCTCGCCATTCTCGACCGCCCGGATAACAACGAGGTGGAATGATGAT
ACCGCACGTTATCGATTTTCGATATCGGAGAGGTGACAAATACGTTAACCTTCTCCGTAC
ATTATCCACGCGCGGAATGGTAAAGTCAGAGTCAGAAATCTCCGGTGGTTAAGATCAC
CGCGTGGCGAACAACGTTTACGGATGTTTAGTCGATGACGTCGAGAGAGAGGTTAA
AGCCGTCCGAGATTGTTGAGCCAACTCGGTGATCGACTCGGTATCTCCGTAAGTTTCAA
CGTGGTGACGAGTTTACGACTCGGTGATCTGAATCGTGAATCTCTCGGTGTGATCCCGA
CGAGACTTTGGCTGTGAACCTTAGCTTTCAAGCTTTATCGTGTTCGCGAAGAGCGGTATG
CACGGAGAAATCCAGAGACGAACCTTCTCCGCGCGTGAAGGACTTAAACCGCGCGTGGT
TACTCTAGTGAGCAAGAAATGAATTCGAATACGGCCCGCTTTTAGGGAGAGTGAGTGA
GTCATGCGGTGTTACGGTGGTGTGCTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
TTCCGACCGTGGCAAGTTGAGGAAGGAATTTGGCCGGAAGCTAGTAAACCGCGTGGCGTG
CGAAGGAATCGATCGTATAGAGCGGTGCGAGGTGTTCCGGAAATGGCGAATGCGGATGAG
CATGGCTGGGTTTGAGTTAATGCCATTGAGTGAGAAGATAGCGGAGTCGATGAAGAGTCG



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TGGAACCGAGTCCACCCGGGCTTTACCGTTAAAGAAGATAACGGAGGTGTGCTTTGG
TTGGATGGACGGGCACTCACTGTCGCATCCGCTTGGCGTTAACTTCACACACTCTTTT
TTTCTTCTATTATTACCATATTATTATTATTTCGAGATTATTCGATATTATTATCA
TTGTGATTTTCCGTTTCGAAAAGTGTAAGGATCTTATGTACAAAGAAAAGAAAGACT
TTTATGTTTTTCTAATAATAAAGAAAGAGTGATTGGGTTCAAAAAAATAAAAAA
AAAAAA

FIG.16F-2

SRPa8 (10964)

TGCATACACGCCGTTTTTCGTAACACGGTTTCGCGAAGCTCTATTTTCATTTCTCCTC
GATTTTGACATGCTTGAGACAATTGTGCCACGAGAACGACGAGAGGATGTTCTTGA
GATGGAGGCTTTGGGAGAGAGGCACTGAATGTGATTGCTTGCAGAGGTTGGGAAAGAGT
GGAGAGGCTGAGACATACAGCAGTGCGCACGTACGGGCTATGAGGTCAGGGTTGGTGCA
GGTCCATTTGACCCCAAGCATTATGAAGACATCGCTGCATAAGGTCACACATTTTACCA
CAAGGATTTTGTGATCGATCAAGATAACCGGTGGCTCTTGCAAGGCTGGAAGGGAAGAAC
TGTCATGGCTCTTTCTGTTTGGAAACCAGAGTCCAAGGCTTGACCGAGAAATCCTCGTTG
GCATATGAGAGACCATCTCTGTGATTTTCTTCCGTGTAATTCCAGAGACAGAAATTACAG
ATGTAAGAAGAGAAATGCTGCCACAAAGAACTTGTTCAAAGATAATTTGATGTAAGTCCTG
TTTTATAACTTTCAGCTGTGTTTTTGTGTTTCTCAGCTAGATTCTCCTAACGGTATTC
TTGTAGCTAGGGTGATCAGATTGTTTGTATATTGCTAGCAGAGTTAGTTGTCTAGATTG
TAAACATATAAGAGGGAAGCTTAGAGTTTCTATGGTTTAAAGAGAAAGTTTTTCTCTC
CAATGTAAAAAATAAAAAA

FIG. 16G



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SRPa10 (11261)

AAAAATGGGAAACCATCACTCTTGATGAACCTTATGATCAATCCAGGAGAGACAACGGTC
GTCAACTGCATTTCATCGGTTACAATACACTCCTGATGAAACTGTGTCTATGACTCTCCA
AGAGACACGGTTCTGAAGCTATTCAAGAGATATCAATCCTGACCTCTTTGTGTTGCAGAG
ATTAAACGGAATGTACAACCTCTCCTTTCTTCATGACGAGGTTCCGAGAACGCGCTTTTTCAT
TACTCTTCACTCTTTGACATGTTTGACACCAATACACGAGGATGATACAAAAC
AGTCACTGTTGGAGAGAGAGTTACTTGTGAGAGACCGGATGAGCGTGTATTTCTGCGAG
GGTGAGAGCGGTTTGCAGGCCCTGAAACCTACAAAGCAATGCGAGTTAGGATTTTGAGA
GCCGGGTTTAAGCCAGCAACTATTAGCAACACAGATCATGAAGGAGGCTAAGGAAATTGTG
AGGAAACGTTACCATAGAGATTTTGTGATCGATAGCGATAACAATTGGATGCTTCAAGGA
TGGAAAGGAAGATCATCTATGCTTTTCTTCTGCTGGAAACCTGCTGAGAAAGTTCAACAAC
AATAATTAAACATCTGAAATAATGTTACTTCTCAATTACATCATTTTGTGTTTCCCAATGG
TTTGTAGAAATATGTTTGTATCCCGTGAGTGGATGCAACTCTTTTTCCTGCAAGTACATA
TTGTATTCAAATCCCTTGTGGAATGATAAATTGTTTAAATCAAAAAA

FIG. 16H



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SRPal1 (18652)

CGGAATGTTGAGATCTTGGAAGCAATAGCTGGGAAACCAGAGTCCACATTATCGATTTT
CAGATGCA CAGGATCA CAATACATGTTT TGGATTCAGGAGCTTGCGAAACGCCCTGGT
GGCCCGCGTTGCTGCGTGTGACGGTGTGGATGATTCA CAGTCCACCTATGCTCGTGGG
GGAGGACTCAGCTTGGTAGGTGAGAGGCTTGCAACTTTGGCGCAGTCA TGTGTTCCCG
TTTGAGTTTCA CGATGCCATCATGCTCTGGGTGCAAGTGCAGCGGGAACATCTCGGGTTG
GAACCTGGCTTTGCTGTTGTGAACTTCCCATATGTATTACACCATGCCAGACGAG
AGCGTAAGTGTGAAATAACAGAGACAGGCTGCTGCATCTGATCAAGAGCCTCTCCCCA
AAACTGGTTACTTAGTAGAGCAAGAAATCCAAACACAACACCTCGCCATTGGTGTCA CGG
TTTGTGGAAACACTGGATTACTACAGCGATGTTTGTAGTCGATGATGCAGCACGGCCA
CGGATGATAAGCAGAGAAATCAGCGCAGAACACACTGTGTAGCAAGAGACATAGTGAAC
ATGATAGCATGTGAGGAGTCAGAGAGAGTAGAGACACGAGGTACTGGGGAATGGAGG
GTCAGAATGATGATGGCTGGGTTCA CGGTTGCGCGGTGTCAGCACATCTGCAGCGTTTGCA
GCGAGTGAGATGCTGAAAGCTTATGACAAAATACTAACTGGGAGGCCATGAAGGAGCG
CTCTACCTCTCTGGAAGAGACGACCCATGGCTACATGTTCCGTGTGGAAGCCAAACCCA
AACTATATTGGGTAAGTTATAGTGATGTTACTTTGAGTGGATAAAGAGAGCACAAAC
AAAAACACATCTGTCGCTGTAATTTT TTAGGATGTGCAATGATGTTTAAAGTTGTAACA
CAACCTAAGTTATATATGTATACAAACCAACCTGGTGTGTTTTCTCTTGTAAATTG
TCATGTGTTGTGGTGGAGCTAGTAATGAATAATAACCAAAACATTGATTAGGTCAA
AAAAAAA

FIG. 16I



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SRPa12 (23196)*

TCTTACTCAAGGTTCTTTTGTCTATCTTGTGCGGAATCCACAAGAGGAGAATAAAGA
TTCGACCTTTATAGATATTAACGACTCTGGATTTTGGGTTTGTGGAGTTGGATCCACA
TGGGTTCTTATCCGGATGATTCCCTGGATCCATGACGAGTTGGATTCAATAAGGACT
TTGATTTGCCCTCCCTCAAAACCAACCTTAGGTTAGCTAATGGGTTCTATTTAGATG
ACTTAGATTTCTCATCCTTGGATCCTCCAGAGGCATATCCCTCCAGAAACAACAACA
ACAACATCAACAACAAGCTGTAGCAGGAGATCTGTTATCATCTCATGATGACGCTG
ATTTCTCTGATTTCTGTTTGAAGTATATAAGCCAAGTTCTTATGGAAGAGGATATGGAAG
AGAAGCCTTGATGTTTTCATGATGCTTTGGCTCTTCAAGCTGCTGAGAAATCTCTCTATG
AGGCTCTTGGTGAGAAAGACCCCTTCTCGTCTTCTGCTTCTGCTGATCATCCTGAGA
GATTGGCTAGTCATAGCCCTGACGGTTCTTGTTCAGGTGGTCTTTTAGTGATTACGCTA
GCACCACTACCACACTTCTCTGATTCTCACTGGAGTGTGATGGTTGGAGAAATAGAC
CTTCTTGGTTACATACACCTATGCCGAGTAATTTTGTTCAGTCTACTTCTAGGTCCA
ACAGTGTCACCGGTGGTGGTGGTGGTAATAGTGGGTTTACGGTTTCAAGTTTGGCG
ATGATTTGGTTTCGAATATGTTTAAAGATGATGAATGGCTATGCGATTCAAGAAAGGGG
TTGAGGAAGCTAGTAAGTTCTTCTTCTTCAAGTCTTCTCAGCTCTTTATTGATGTTGATGTT
ACATCCCTATGAATTTCTGGTTCCAAGGAAATGGTTCTGAGGTTTGTGTAAGACGGAGA
AGAAAGATGAGACAGACATCATCATCATCATAGCTATGCACCAACCAACAGATTAA
CTGGTAAGAAAGCCATTGGCGGACGAGATGAAGATTTCGTTGAAGAAAGAGTAACA
AGCAATCAGCTGTTTATGTTGAGGAAAGCGAGCTTTCTGAAATGTTTGATAACATGTTCC
TATGTGGCCCTGGGAAACCTGTATGCATTTCTTAACAGAACTTTTCTACAGAAATCCGCTA
AAGTCGTGACCGCACAGTCAAATGGAGCAAAGATTCTGTTGGAAGAAATCAACTTCTACTA
GTCAATAGTAACGATTCTAAGAAAGAACTGCTGATTGTGAGGACTCTTTTGGTGTATTGTG
CACAAGCTGTATCAGTGGATGATCGTAGAACCGCCAACTGTTAGCTAAGGCAGATACGAG
AGCATTTCTGCTCTAGGCAATGGTTTCAAGCGGTTGGCTCATTTATTTGCAAAATAGTC
TTGAAGCACGCTTAGCTGGGACCGGTACACAGATCTACACCGCTTTATCTTCGAAGAAA
CGTCTGCAGCAGACATGTTGAAGGCTTACCAGACATACATGTCGGTCTGCCCCTTTCAAGA
AAGCTGCTATCATATTGCTAACCAACAGCATGATGCGTTTCACTGCAACGCCAACACGA
TCCACATAATAGATTTTCGGAATATCTTACGGTTTTCAGTGGCTGCTCTGATTCATCGCC
TCTCGCTCAGCAGACCTGGTGTTCGCCCTAAGCTTCGAATTAACGGTNNNNNNNNNN

FIG.16J-1



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NNNNNNNNNNNNNNNNNGAGTTCAGGAGACAGGTCATCGCTTGCGCTCGATACT
GTCAGCGACACAAATGTTCCGTTTGAGTACAAACGCAATTGCTCAGAAATGGGAAACGATC
CAAGTCGAAGACTTAAAGCTTCGACAAAGGAGAGTATGTGGTTGTGAACCTCTTTGTCCGT
TTCAGGAAACCTTCTAGATGAGACCCGTTCTGGTAAACAGCCCGAGAGATGCAGTTTGAAG
CTGATAAGAAATAAACCCGAATGTCTTTCATTCACGCGATCTTAAGCGGAATTACAAC
GCGCCATTCTTTGTCAACGAGGTTTCAGAGAGCGTTGTTTCACTTACTCGGCTGTTTGAT
ATGTGTGACTCGAAGCTAGCTAGGGAAGACGAGATGAGGCTGATGTATGTGTTGAGTTT
TATGGGAGAGAGATTGTGAATGTTGTGGCTTCTGAAGGAACAGAGAGAGTGAGAGCCGA
GAGACATATAAGCAGTGGCAGCGGAGACTGATCCGAGCCGGATTTAGACAGCTTCCGCTT
GAGAAGGAACCTGATGCAGAACTCTGAAGTTGAAATCGAAACGGGTACGATAAAACTTC
GATGTTGATCAAAACGGTAACTGGTTACTTCAAGGGTGGAAGGTAGAAATCGTGATGCT
TCATCTCTATGGGTTCCCTTCGCTTTCATAGATGTGTTGTTTCTTACGTTCTAAGCGACTGG
ATTTATGTAGGGCTTTTCTGTGTAGTCTCTCGCCCAACACGAGTGGATTAAAGTTCAGAG
TTAGGGTTCTTGAACTAGAAATGTTGTTATATTATGCTTGTGACATAGCGTGTGAAGA
GTGTAGCCCTAAGAGATATAGTACTCATTCATGTCATGATCTTTTGCTATATGTTNCATGT

FIG. 16J-2



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SRPd1

TCTGCAGACAAATTTNAGGAGGCCAATACCATGCTATTGGAAATTTTCAGAACTG
TCCACACCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTACTTCTCAGAGGN
AATGTCGGNNAGATTAGTTAGCTCCTGCTTAGGAAATCTATGCTTCTCTTCCNGC
AACAGTGGTGCCTCCTCATGCTCAGAAAGTGGCCTCA

FIG. 16K

SRPg1

TCAACTGAGAAATCTAGAAGATGCCAACAAAGATGCTTCTGGAGATTTCTCAGTTA
TCAACACCGTTCNNCACTTCAGCACAGCGTGTGGCAGCATATTTCTCAGAAGCC
ATATCAGCAAGTTGGTAGTTTCATGTCTAGGGATATACGCAACTTTGCCACAC
ACACACCAAGCCACAAAGGTAGCTTCAGCTTTTCAAGTGTTCATGGTATTAGT
CCTTTAGTGGAGTTCTCACACTTCACAGCAAAACCAAGCAATTCAAGAAGCCTTC
GAAAGAGAAGAGAGGGTGCCATCATAGATCTTGATATAATGCAAGGGTTG

FIG. 16L



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SRPp1

TCTGCAGACAACTTTGAAGAAGCCCAATACAATACTGCCCTCAGATCACAGAACTC
TCCACCCCTATNGCAACTCGGTGCAACGAGTGGCTGCCCTATNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNTGCATAGGAATGTATTCTCCTCTCCCTCCT
ATTCACATGTCCCGAGCCAGAAAATTGTGAAT

FIG. 16M



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FIG. 17A-1

Partial DNA sequence of ZCARECROW gene

GATATCAGCATCATCAATTTAAATGTAAGTTGGCAAAAGATCATGAGGGTTCTCATAGT
AATTTGGCCACAAGGTATGACACTGTCTCAATTGAGCAATCTAGTAGAGAAACTGATCCA
TCATATATTGCTCATATTGAAAGTGAAAAGATATGCTCAAGAACCTAGTAGAGAGCTA
AAAATTGAAAAATCTAGCTCTACTAGAAAAATATGATAGTTGCCCTGTTTCTCATGAAAA
TTTATTAGATAATCATATCATGCTAGATGTCGCTCATGAGGTTGTTCTTGCTAGTTTAG
ATTCCTGTGGGCATTTCATCTCTTTTAGATGCACCTAACATGATAGGAAGTTTCTAATCTGG
TGCTTCACAATCTGGTGATTTCATGCTTCTTCATTGCAATTGATGATTGATGCTTGATTC
ATGCTTCAGTCACCTTTGTGCGTTTAATTGGTATTGTATGTATCATCTAGATTGTAGGGTGT
CTGCAACTAGTGTTCACCATGTGGTTTTTTTAGTATCATCTCGTATTAGTTTCTAACTTTC
TATTGATATATTAAGTGATAACTAGTTTTAGAAATATTCTTTGTGCCATTAAATGCTAC
AACTTGTTTTAGCGTGACGTAGCATTAATAATTTCCTTATTATGAAGCGGAAGAG
AAACGCGCCCAACAGAGCATCCACGTCTCATTTTACCTTCATCTCGTTGGATCATAGA
TGAGCGGTCCACGGTGAACTCCGTTTGCCCTGCAAAACACAGTCCCTCTACGCGCTGTTAAG
TAGCTTCTAGAAACATACGATGTGTCCGTCCTTCTTTAGGAGGAGCCGGATCCGGC
GCCGAGTCCGCCAAGTCCGACCGCGCGGCTCGGCGCGCGCGCGCGCGCGCGCGCGGAA
GGAGTGACGCGGGGAGAGCGGCGGACGAGGAGGCGCTCCACCTGCTGAGTGTGACGC
TGCTGCTCAGTGCGCGGAGGCGCGTGAACGCGGACAACTCGACGACGCGCACCCAGACGC
TGCTGGAGATCGCGGAGCTGGCCACGCGGTTGCGCACCTCGACCCAGCGGTGGCGCGCT
ACTTCGCGGAGGCCATGTGCGCGCGTCTGTCAGTCTCTGCTAGGCTGTACGCGCGCG
TGCCCGCGGCTCCCCCGCGCGCGCGCTCCACGCGCGCGTGGCGCGCGCGGTTCCAGG
TGTTCAACGGCATACGCCCTTCGTCAAAGTTCTCGCACTTACCGCGCAACCCAGGCCATCC
AGGAGGCGTTCGAGCGGGAGGAGCGGTGTCACATCATCGACCTCGACATCATGACGGGC
TGAGTGGCGCGGCTCTTCCACATCTTGTCTCCGCGCGCGCGCGCGCGCGCGCGGTCA
GGCTACCGCGCTGGGGCGTCCATGGACGCGCTCGAGGCGGCGGGAAGCGCTCTCCG
ACTTCGCGGACACGCTCGGCGCTGCCCTTCGAGTTCTGCGCGCTCGCGGAGAGCGCGCA
ACGTTGACCGCGAGAGCTGGGCGTCACGCGCGGAGGCGCGTCCGCTCCACTGGCGCGC
ACCACTCGCTTACGACGTATCGGCTCCGACTCCAAACACGCTCTGGCTCATCCAAAGGT
CCTCCATTTCTCTGCGCTTCTTCCATGTCAAAATCTTGATGCAATCATGACCACTT
TTCAGCTGCTGACATTGGATAATGTGAGCTTTACGGCAAGCATCAAGTCTGTTAGTACA



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TCCATTACAGCTATTTCTAAATAATCTTCGGAGGTTTCCTGCTCATAGTAAAAAAAT
CGCGTTTGAAGCTCAAAAGCGATTCTTCGAGGTTTGCTGTTGAGCGCTATTTTGGGA
AACCCCATTTTCTCAATTGATTTTATTTTAAAGAAAAATAGTTCATTTTCTCTTG
TGAATGAGTCCCCAACTAACCCCTAATATAAAAAAAGCGCTTTGGAGCTCAAAACG
CTCGTTGTTATGACCAACGAGCTTATAGGTTTAAAAAGGTTGAATCTTGACAAATGCTTT
TGAAAAGGTTGAATCTTGACAAATGCTTTTGAGATGATACTGTAGTGTAGTCTGTAGTGGA
GCATCCTCCATGGTCTTTGGTGATCGAGAATTCCCTGCAGCCCCGGGGATCC

FIG. 17A-2

Partial amino acid sequence of ZCARECROW protein

YQHHQFXMXVKRSXGFSXXFGHKVXHCXNXXAIXXRNXSIIYCSYXXKRYAQEPSREAK
NXKIXLYXKNMIGCLFLMKIYXIIISWLDVAHEVVLASLDSCGHSSLLDALTXXEVSNLV
LHNSGDSCLHCNXXYXCLIHASVTLCVXLVYVSLDCRVSATSVSPCGFLVSFVLVSNFL
LIYXSDNXFXKYSLVPLMLQLVFSVYVSIIFPYYESGRETRPTRASTSSHFTFIVGSXM
SGPRXTPFACKTTSSTRCXVASRNITMCPVHSFRRSRIRRRSRPRSRPPRPPRPPRSGR
RCSGGSSATRRASTCXVLTLLLOCAEAVNADNLDDAHQTLLLEIAELATPFGTSTQORVAA
FAEAM SARVVSSCLGLYAPLP PGSPAAARLHGRVAAAFQVFNIGISPFVKFSHFTANQAIQ
EAFEREERVHIIDLDIMOGLOWPGLFHLVSRPGGPPRVRLTGLGASMDALEATGKR
FADTLGLPFEFCVAEKAGNVDPOKLGVTRREAVAVHWPHSLYDVIGSDSNTLWLIQRS
SIFLLCLSSMSNLDAIMTTFQLLLTDNVSTASIKSWXYIHYSYFXNILRRFFPAHSKKKS
RFEAQKAISSSEVCCXALFWKPHFLNXFLFFKEKLVHFSLVKWSPKLTLILKKTFRFGAQN
RCYDOPALXVXXGXILTMLLKRNLNDNAFEMILXCSLXWSILHGLWXSRIIPAARGI

FIG. 17B



302 349
SCR SADNLEEANKLLLEISQLSTPYGTSAQRVAAVFSEAMSARLLNSCLGI
SRPd1 SADNFxEANTMLLEISELSTPXXXXXXXXXXYFSXXMSXRLVSSXLXI
SRPg1 STENLEDANKMLLEISQLSTGXXXXXXXXXXXXXXXXXXXXXSCSLGI
SRPp1 SADNFEEANTILPQITELSTPYXNSVGRVAAYYYYYYYYXXXXXXCIGM

350 396
SCR YAALPSRWMPQTH-SLKMVSAFQVFNGISPLVKFSHFTANQAIQEAFE
SRPd1 YASLPATVVP--PHGQKVAS
SRPg1 YATLP-----HTQSHKVASAFQVFNGISPLVEFSHFTANQAIQEAFE
SRPp1 YSPLPPIxMSQ----SQKIVN

397 412
SCR KEDSVHIIDLDIMQGL
SRPg1 REERVHIIDLDIMQGL

FIG. 18

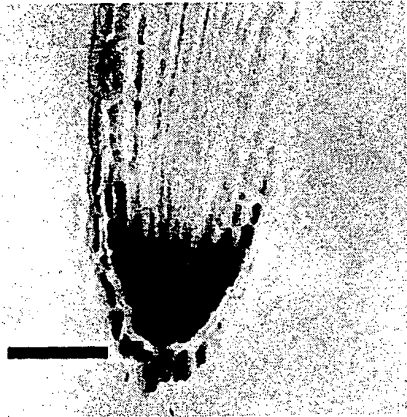


FIG. 19A

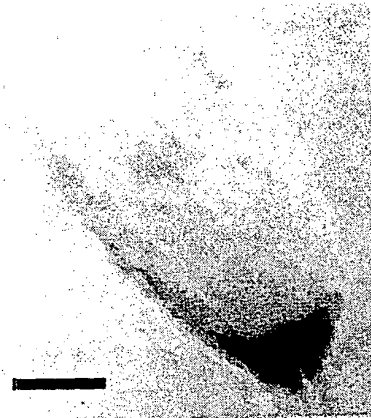


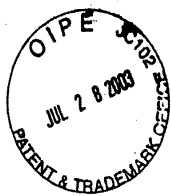
FIG. 19C



FIG. 19B



FIG. 19D



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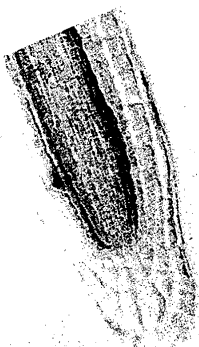


FIG. 19E

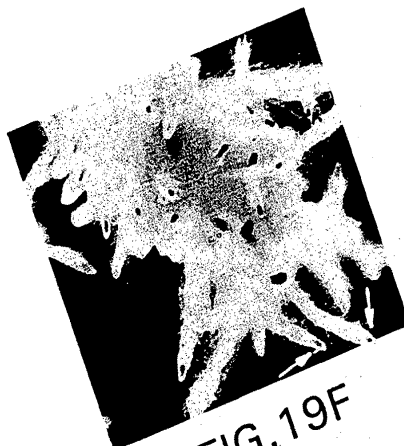


FIG. 19F

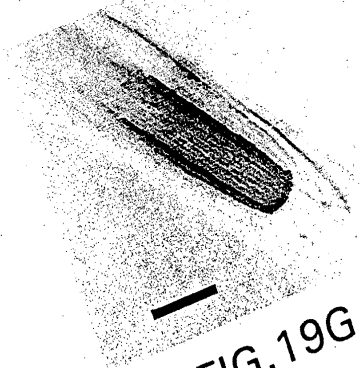


FIG. 19G



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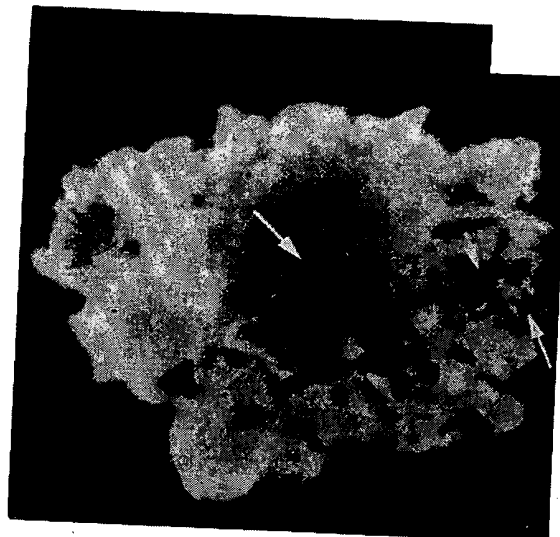


FIG.20A

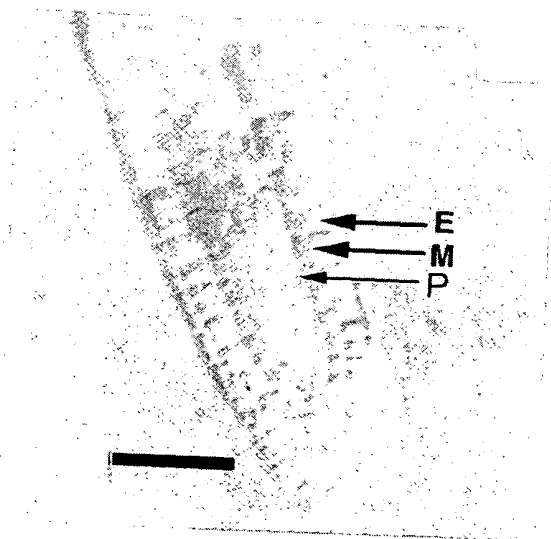


FIG.20B

SCR Promoter::GUS



FIG.21A

SCR Promoter::SCR 73/100



FIG.21B

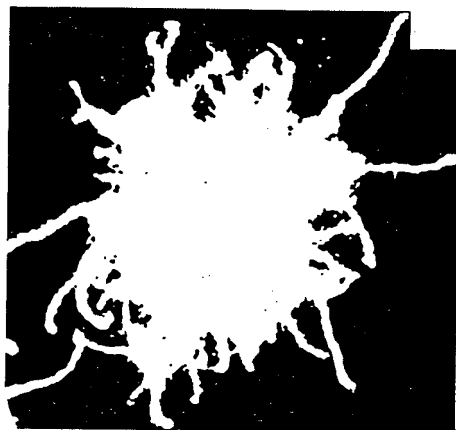


FIG.21C

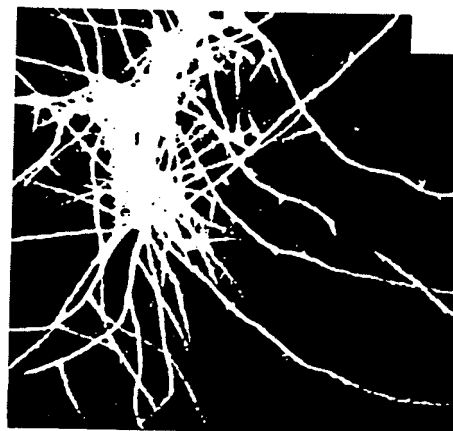


FIG.21D



FIG.21E

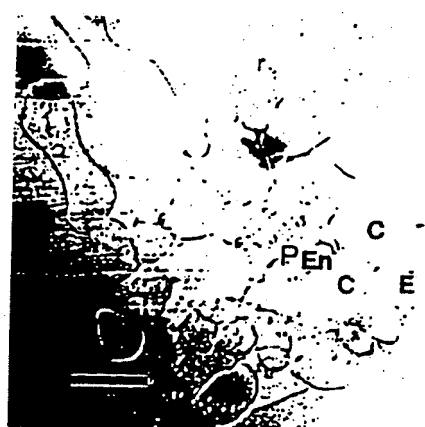
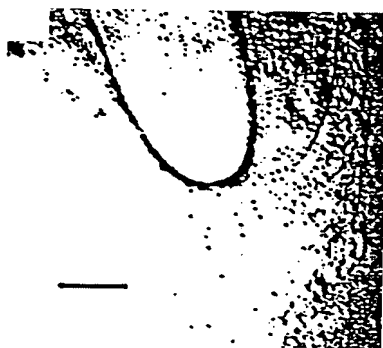
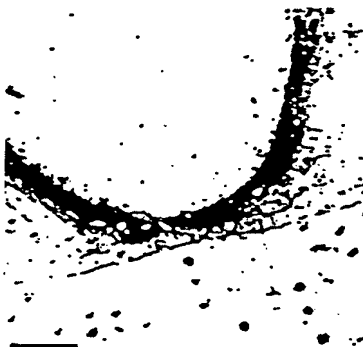


FIG.21F



Maize primary root

FIG.22A



Maize primary root

FIG.22B



Maize primary root

FIG.22C



Maize embryo

FIG.22D



FIG.22E



Maize lateral root

FIG.22F

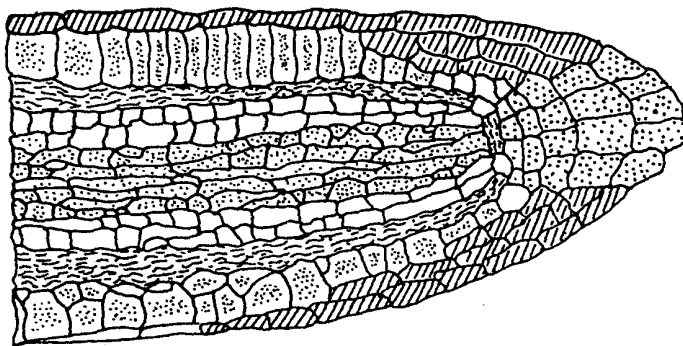


FIG. 23B

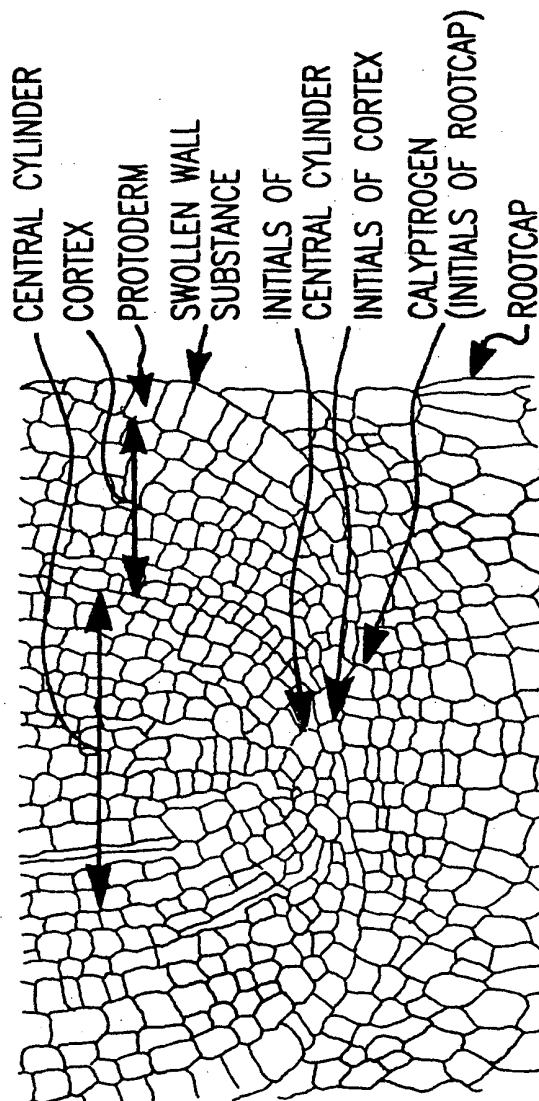


FIG. 23A

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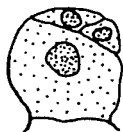


FIG. 24A



FIG. 24B

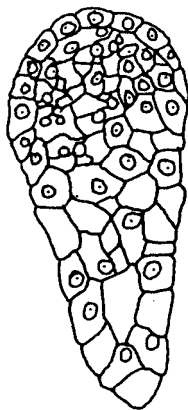


FIG. 24C

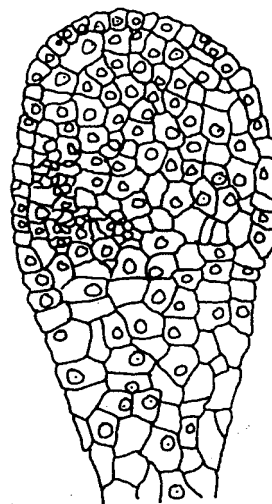


FIG. 24D

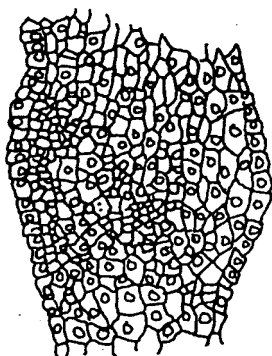


FIG. 24E



FIG. 24F

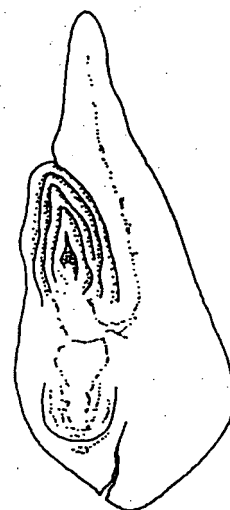


FIG. 24G



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ctgctagctcagcctactcactccactcaactcaccaccaactccactccgctcccgagc 60
ccggactgactgactgactgtggtggtggtggtgcatcagcagcccgcgcgccgcaaaa 120
cacgcaaactgctccctccctcactcaccctatcccccgcgctgggtcgcccgatcgcc 180
atgcgcgcggcggttctctcttggtgtttctagatgggctcctcctcctcctcctcttc 240
tcctcgctcctcctccgcccgcgcatccaccgccccccactcctttccccactctcATGCCACC 300
1 M P P
GCCACCGCCTCCGCCTCCTCTCACTCCTTATTGCCGCCGCTGCCCTCCCCACACCTCCC 360
4 P P P P P P L T P Y C R R C P P P H L P
TCCGCCTCCTCCTTCTTCCCCAAACCACTTCTCCTCCACTACCTCCATCAGCTAGACCA 420
24 P P P P S S P N H F L L H Y L H Q L D H
CCAAGAAGCCGCCGCCGCCGCGCCATGGTCCGCAAGCGCCCCGCGTCCGACATGGACCTCCC 480
44 Q E A A A A A M V R K R P A S D M D L P
GCCGCCGCGCCGCCACGTACGGGCGACCTCTCCGACGTACGGCGGGCGCTGCCGCCGG 540
64 P P R R H V T G D L S D V T A A A A A G
TGTTGGTGGTAGTGGCGCGCGTCTCCGCCAGCGCGCAGCTGCCCGCGCTGCCACCCA 600
84 V G G S G A P S S A S A Q L P A L P T Q
GCTCCACCAGCTGCCCCCGCGTTCCAGCACACGCGCCGGAGGTGGACGTGCCCGCGCA 660
104 L H Q L P P A F Q H H A P E V D V P A H
CCCGGCCCGGCCGCCACGCGCAGGCGGGCGGCGAGGCAACCGCGTCCACGACCGCGTG 720
124 P A P A A H A Q A G G E A T A S T T A W
GGTGGACGGCATCATCCGCGACATCATCGGGAGCAGCGGCGGCGCGGTCTCCATCAC 780
144 V D G I I R D I I G S S G G A A V S I T
GCAGCTCATCCACAACGTCCGCGAGATCATCCACCCCTGCAACCCCGGCTCGCGTCGCT 840
164 Q L I H N V R E I I H P C N P G L A S L
CCTGGAGCTCCGCCTCCGCTCCCTCCTCGCAGCCGACCCGGCCCCACTGCCGCCGCCGCC 900
184 L E L R L R S L L A A D P A P L P P P P
GCAGCCGAGCAGCATGCTCTCCTGCACGGCGCTCCGGCCGCGCTCCCGCGGGGCTGAC 960
204 Q P Q Q H A L L H G A P A A A P A G L T
GCTCCCTCCCCGCCACCGCTTCCGGACAAGCGCCGCCACGAGCATCCACCGCCGTGCCA 1020
224 L P P P P P L P D K R R H E H P P P C Q
GCAGCAACAGCAGGAGGAACCGCATCCGGCGCCGCGAGTCGCCCAAGGCCCGACCGCGGA 1080
244 Q Q Q Q E E P H P A P Q S P K A P T A E
AGAGACCGCAGCGGCGGCGCGCCGCCACAAGCAGCAGCTGCTGCGGCCGCCAAGGAGCG 1140
264 E T A A A A A A A Q A A A A A A A K E R
GAAGGAGGAGCAGCGGCGGAAGCAGCGGACGAGGAGGGCCTCCACCTGCTGACGCTGCT 1200
284 K E E Q R R K Q R D E E G L H L L T L L
GCTGCAGTGCGCCGAGGCCGTGAACGCGGACAACCTGGACGACGCGCACCGAGCGCTGCT 1260
304 L Q C A E A V N A D N L D D A H Q T L L

FIG.25A



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GGAGATCGCGGAGCTAGCGACGCCGTTTCGGCACCTCGACGCAGCGCGTGGCCGCCTACTT 1320
324 E I A E L A T P F G T S T Q R V A A Y F
CGCGGAGGCCATGTCTGGCGCGGCTCGTCAGCTCCTGCCTGGGCCTGTACGCGCCGCTGCC 1380
344 A E A M S A R L V S S C L G L Y A P L P
GCCGGGCTCCCCGCGCGGCGCGCCTCCACGGCCGCGTCCGCCGCGGTTCCAGGTGTT 1440
364 P G S P A A A R L H G R V A A A F Q V F
CAACGGCATCAGCCCCATTCTGTCAGTTCTCGCACTTCACCGCCAACCGGCCATCCAGGA 1500
384 N G I S P F V K F S H F T A N Q A I Q E
GGCGTTTCGAGCGGGAGGAGCGCGTGCACATCATCGACCTCGACATCATGCAGGGGCTGCA 1560
404 A F E R E E R V H I I D L D I M Q G L Q
GTGGCCGGGGCTCTTCCACATCCTTGCTCCCGCCCCGGGGGGCCCCAGGGTGAGGCT 1620
424 W P G L F H I L A S R P G G P P R V R L
CACCGGCCTCGGGGCGTCCATGGAGGCGCTCGAGGCCACGGGGAAGCGCCTCTCCGATTT 1680
444 T G L G A S M E A L E A T G K R L S D F
CGCCGACACGCTCGGCCTGCCCTTCGAGTTCTGCGCCGTCGCCGAGAAGGCCGGCAATGT 1740
464 A D T L G L P F E F C A V A E K A G N V
TGACCCGGAGAAGCTAGGGGTCACGAGGCGGGAGGCCGTCGCCGTCCACTGGCTGCACCA 1800
484 D P E K L G V T R R E A V A V H W L H H
CTCGCTCTACGACGTCACTGGCTCCGACTCCAACACGCTCTGGCTCATCAAAGgtagga 1860
504 C L Y D V T G S D S N T L W L I Q R
aggagtacaccatctctcgatcctgacttccttgctaccatgtcaaactcttgatgcaatc 1920
atggccacttttcagctactaacacttttagtttagccaatgcgacatccagtacaactaa 1980
tctaaaaaaataatcttcagaggtttcctagtaaaaaaacgcgtttttggagctcaaaa 2040
agcttgatcattatgaccaaccaactttctaggcttaaaaagggtgaatcttggcaatgct 2100
tttgagacgatgctgtactgaagtactggtagagagagtatcctccatggcctttgttga 2160
tcccagaaccacaaaagatagtagtttcgctcgcattttggttagtgagggtgttctgatca 2220
tcacttgaggatggagctgaaagttcctatcatcatgaccaactttccatggcaaaagg 2280
tttctagttccaagtggcaggacgatgattactgagtgaatggagtaactgtcatc 2340
ttctaccactaaccatcatttattaatacataaatcatcatccggagcctaaactcagaa 2400
aggctaatacaaaagtgaatctttctcaaatggctgccatattgccagtgggtacatgcctg 2460
gccattgtactttttcggatgaaccatctcgtctcaagcatgagatgaaggcctgaactgc 2520
aatgtccttgatttgatgcaaccattattagaagaaacgctaagcgatgccggtcctggc 2580
aagggaatgccatatcgtcagacagacagggttcggaatcgaatggctagctggtgac 2640
aatcgcacggggaattaataaactacattggtcattgattccatccccacacacctgca 2700

FIG.25B



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gGCTGGCCCCCAAGGTGGTGACAATGGTGGAGCAGGACCTGAGCCACTCGGGCTCCTTCC 2760
522 L A P K V V T M V E Q D L S H S G S F
TGGCGCGCTTCGTGGAGGCCATCCACTACTACTCGGCGCTGTTGACTCGCTGGACGCGA 2820
541 L A R F V E A I H Y Y S A L F D S L D A
GCTACGGCGAGGACAGCCCCGAGCGGCACGTCGTGGAGCAGCAGCTGCTGTGCGGGGAGA 2880
561 S Y G E D S P E R H V V E Q Q L L S R E
TCCGCAACGTGCTGGCCGTGGGCGGGCCGGCCCGCACC GGCGACGTCAAGTTCGGCAGCT 2940
581 I R N V L A V G G P A R T G D V K F G S
GGCGCGAGAAGCTGGCGCAGTCCGGGTTCCGCGCCGCCTCGCTCGCCGGCAGCGCCGCGG 3000
601 W R E K L A Q S G F R A A S L A G S A A
CGCAGGCGTCCCTGCTGCTCGGCATGTTCCCTCCGACGGGTACACGCTGGTGGAGGAGA 3060
621 A Q A S L L L G M F P S D G Y T L V E E
ACGGCGCGCTGAAGCTCGGGTGGAAAGACCTCTGCCTGCTCACC GCGTCGGCCTGGCGCC 3120
641 N G A L K L G W K D L C L L T A S A W R
CCATCCAGGTGCCGCGGTGCCGTTGATgagacctctgcctgctcctgcttgcttgagag 3180
661 P I Q V P P C R *
gccgccactccacttgttttgcatctgtagctgctcggtttggtcatcagctgggagata 3240
agaaaagcggaacgtactaattgctctggagtagatccatccattcacagtgatagtta 3300
ctgatgtactaagctttaattagttcaatgctagatcggttcttggttcaggtgtcgatcgc 3360
gtatccttgctccttggtctccttttcattttggtgctttgtctagtcgctttcccgacta 3420
atgccgtgctcttcatgcgcgttctagtgagattcttgccgagaatattagcatagttt 3480
tcatgtaaagtagccatcaagcaagtatta 3510

FIG.25C



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```
***** * ***** ***** ***** *** ***** *
Zm SCR EAVAVHWLHH SLYDVTGSDS NTLWLIQRLA PKVVTMVEQD LSHSGSFLAR 543
At SCR EAVAVHWLQH SLYDVTGSDA HTLWLLQRLA PKVVTVVEQD LSHAGSFLGR 533

***** ***** ***** * * ***** ***** ***** *
Zm SCR FVEAIHYYS A LFDSL DASYG EDSPE RHVVE QQLLSREIRN VLAVGGPART 593
At SCR FVEAIHYYS A LFDSL GASYG EESEERHVVE QQLLSKEIRN VLAVGGPSRS 583

* *** ***** * * ** ***** ** ** ***** ***** **
Zm SCR GDVKFGSWRE KLAQSGFRAA SLAGSAAAQA SLLLGMFPSD GYTTLVEENGA 643
At SCR GEVKFESWRE KMQQCGFKGI SLAGNAATQA TLLLGMFPSD GYTTLVDDNGT 633

***** * ***** *
Zm SCR LKLGWKDLCL LTASAWRPIQ VPPCR 668
At SCR LKLGWKDLSL LTASAWTPR- ----S 653
```

FIG.26A-2



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FIG.27A

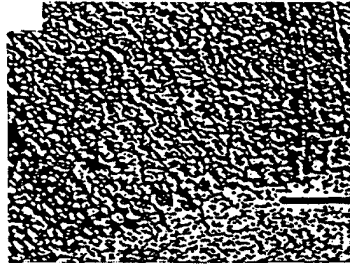


FIG.27B



FIG.27C



FIG.27D

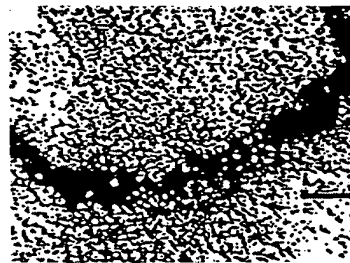


FIG.27E



FIG.27F

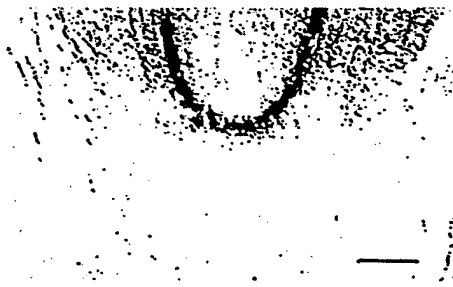


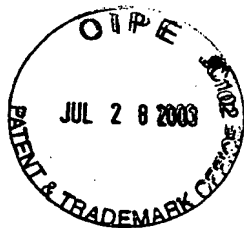
FIG.27G

96H



FIG.27H

100H



83/100

ctttgtcaat ggtaaatgag ctgaggcaga tagtttctat ccaaggagac ccttctcaga
61 gaatcgagc ttacatggtg gaaggtctag ctgcaagaat ggccgcttca ggaaaattca
121 tctacagagc attgaaatgc aaagagcctc cttcggatga gaggcttgca gctatgagat
181 cctgtttgaa gtctgccctt gtttcaagtt cgggttttta gcagctaata gtgcgatact
241 tgaagcaatc aaaggtgaag aagaagttca cataatcgat ttcgatataa accaagggaa
301 ccaatacatg aactgatac gaagcattgc tgagttingcc tgggtaaacg acctcgctg
361 aggttaaaca ggaattgatg accctgaatc cagtnccaac cgctccattt gggggggcct
421 aaagaa

FIG.28

gagtacgac ttaaagctat tcccggtgac gcgattctca atcagttcgc tatcgattcg
61 gcttcttcgt ctaaccaagg cgccggagga gatacgata ctacaaaca gcggttgaaa
121 tgctcaaacg gcgtcgtgga aaccactaca gcgacggctg agatcaactc ggcatgttgt
181 cctggttgac tcgcaggaga acggtgtgcg tctcgttcac gcgcttttgg cttgcgctga
241 aagctgttca gaaagagaat ctgactgtag cggantctgg tgaagcaaata cggattctta
301 gccgtttctc aaatcggagc gatgagaaaa gtcgctactt act

FIG.28A-1

aaatttttca attacctaata ataatgaaag ataagatctt aacaagtgac aaagggaaaa
61 acagtaggat ttagtttggc ttcggtcggg aatctatcat cataaccggt tcaacagatc
121 aattcattga gccaccatct aattggtgag agtttccaag ccgaggtggc tatgagcggg
181 cgtgtgtgcc aacccaacat gagacagccg tcaactctct ccaccgata acctcaccg
241 ccgttgaaca gagccaaaag cataactcgt tgcttaaacg cattcgaacc aatatgtgca
301 gccgcaaacc cagcagaccc gaaccggttc ctccantgac ttcaacggtt catgacgggt
361 caacttcggt ca

FIG.28A-2

ttttttttta agtgagaacc ttaacaaatt taaccatttg aactgaaata tgaacatgta
61 aagactcatt cacacttagc aaatagggtt agaaccaaaa ctctaattat ttttatataa
121 tagggaaaaa aaagaaagaa aaattcttcc ataagtgtta gattagcttt tagtacctgt
181 gatcacccct aacctctggt aataatacat ggagatgatt taaccagtta cacaataacc
241 caagattaca gtaaaaacat aattatgttt tatgaaacat aaagactata tgctcttgct
301 acttatctta cctccaagct gaagcaacgg attaagcttt tctcctccca gcaaaaatgg
361 gagtcaccc atttcttctt taaggttgta cttnttgca

FIG.28A-3



84/100

gctatggaag gagagaagat ggttcatgtg attgatctcg atgcttctga gccagctcaa
61 tggcttgctt tgcttcaagc ttttaactct aggcctgaag gtccacctca tttgagaatc
121 actggtgttc atcaccagaa ggaagtgtt gaacaaatgg ctcatagact cattgaggaa
181 gcagagaaac tcgatatccc gtttcagttt aatcccgttg tgagtaggtt agactgttta
241 aatgtagnac agtttagggg ttaaacagga gaggcnttag ccgttagctc ggttcttcaa
301 ttgcata

FIG.28A-4

ccgatcatca aattagttat cttcagctca aattggattt ggtttggtat tacaccaca
61 ccagaccaa ttgaaccaac acacaaaggc tttacatgca gaggcagtag aagcatttaa
121 gccaaaatag cataaagaga cagaaagtca ccatcacaaa acaactaaga ttgtgtcccc
181 atgtatacaa aaaagaaagg gactctgtc ataacaaaaa tagaagacaa actgtaatat
241 atcattcact tcctgcatct ccaagctgat accgagtata gaggtcgatc ttgccagcaa
301 attactgcgc acccgtctc ttccttgatt ctatacccat caaaa

FIG.28A-5

ctggaattac aattacagca atttgattc aattgttgaa tctaagcctg gcttcatctc
61 tttggcctgg aacgatttac ctctcctcac tctttcttcc tggcgataac caaaccaaac
121 cgatccggtg ttcttagttt tgttttgtt tcaatgttat ttttggttag acaaatattc
181 aattgttaat atactccgtg gtcagagtgt tttgttttcc ttttagttcg aacgttgaat
241 taattcaggg gtaggtttt aattctctga acctatgtg ttttttggtg acatcatttg
301 gatttgtgaa ctaggtttta aaactggct tagtcttgtt gttttctcat tagataattt
361 aaactgggtt gcttctttt ttttggttg ggataaaagt gaccgg

FIG.28A-6

gtggaattac aattacagca atttgattc aattgttgaa tctaagcctg gcttcatctc
61 tttggcctgg aacgatttac ctctcctcac tctttcttcc tggcgataac caaaccaaac
121 cgatccggtg ttcttagttt ttgtttgtt ttcaatgtta ttttggtta gacaaatatt
181 caattgttaa tatactccgt ggtcagagt tttgttttn ctttagttc gaacgttgaa
241 ttaattcagg gtaggtttt gaattctctg aacctnatgt gtttntggt aacatcattt
301 ggatttgtga actaggttta aaaactggnc ttagtcttgt tgttttctca ttaggataat
361 ttaaactggt ttgcttctt attttnggtt gggataaagt gaccgg

FIG.28A-7



85/100

caaaactaca tttcatcact tttttgagca aaattacaaa taaaagagta gttacaaata
61 tatttggtt tcaacttcct aattttatga aatagtaatt acatctcaaa cagatgacca
121 gaaccggtca ctttatccaa ccaaaaataa agaagcaaac cagtttaaatt tatctaata
181 gaaaacaaca agactaagac cagtttttaa acctagttca caaatccaaa tgatgttacc
241 aaaaaacaca taagggttcag agaattcaaa acctaccctt ganttaattc aacgttcgaa
301 ctaaaagaaa aacaaaacac tctgaccacg gagtatatta acatttgatt atttgtctaa
361 ccaaaaataa cattgaaaac aaaacaaaac tanggaatac cggatcgggt

FIG.28A-8

cccaacgggt cctgagcttc ttacttatat gcatatcttg tatgaagcct gcccttattt
61 caaatcgggt tatgaatctg ctaatggagc tatagctgaa gctgtgaaga acgaaagttt
121 tgtgcacatt atcgatttcc agatttctca aggtgggtcaa tgggtgagtt tgatccgtgc
181 tcttggtgct agacctggtg gacctccgaa cgtaggata acgggaattg atgatccgag
241 atcatcggtt gctcgtcaag gaggacttgc agtagttgc acaaagcact tggca

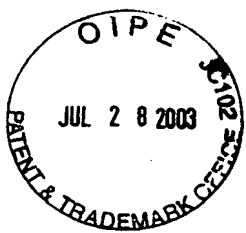
FIG.28A-9

gggtcatcaa catatcactt actactacaa catttgacaa cttgttctn cggatcatgc
61 atgagtttta cttttacaaa cagattctgc aaactttaaa agcaagtttc taatctcttc
121 tgaaccgaa caaggttttt attagttacc tccaagcaca agaagtgata agaggttgat
181 tcttccatcc taaatacaat gctccatctc tttcttcaag tgtatacttc tctgaataac
241 tctcaagcaa tcctttgatt gttgcgttca catacgagct caaaggatac ggtttaaatc
301 ccgccatgtg aaaccgaga

FIG.28A-10

caaaaattta tatatttgtg tgaacttaaa tttaaaaatc catcgactg agcaaaataa
61 nntcagaaac taaaaatttg tcatttaaga taaattgaat taaggaaaat attttttta
121 taattgaaac tccggtggaa atcaggagga gcgacatctc catgctgaaa ctccgacgag
181 ttctgtcctt tgccaacata ggagaagtga gttatgtttc tcctcgacgt gaaagcctct
241 cactggcgtc cgttggnrna aacactcggc ttgagactcc gtgaagttac tgtgcgtcac
301 cggtgagaaa cccatctgta gaaacatcgc ttgccacgtc atcatcggcc tttctatcgg
361 acggctacga tccaacacca gcttctctat ctccggctgt ataaggaaa

FIG.28A-11



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ctattnnac aattnattn gttattagaa gtggtagtgg agtgaaaaaa caaatcctaa
61 gcagtcctaa ccgatccccg aagctaaaga ttctncacct tcccaaataa agcaaaacct
121 agatccgaca ttgaaggaaa aaccttttag atccatctct gaaaaaaacc aaccatgaag
181 agagatcatc atcatcatca tcatcaagat aagaagacta tgatgatgaa tgaagaagnc
241 gacggtaacg gcatggatga gcttctagct gttcttggtt ataaggtag gtcattccgaa
301 atggctgatg ttgctcaga aactcgagca gcttgaagtt atgatgtcta atgttcaagn
361 aagncgggtct ttntcaactt cgcnaactnn gactgttcac tntaatncgg cggnggtttt
421 caacngtggc ttgntttcna tgntnaccga ccttaat

FIG.28A-12

atgggaaagg agcatttaat ctcgactcaa ttgctctacg agctctctcc ttgtttcaaa
61 ctcggtttcg aggccgcgaa tctcgccatt ntcgacgccg ccgataacaa cgacggtgga
121 atnatgatac cgcacgtaat cgatttcaat atcggagaag gtggacaata cgtaaacctt
181 ctcentacat tatccacgag ccggaatggg aaaagtnaga gtcagaattc tccggtggtt
241 aanatcaccc gccgtggcga acaacgttta cgggatgttt agtcggatga cgggtggnga
301 agagaggttt aaaagcccgt ncgngntttt ttttgnagcc actncngntn atccg

FIG.28A-13

actcggatc tccgtaagtt tcaacgtggg gacgagttta cgactcgggtg atctgaatcg
61 tnaatctntc ggggtgnatc ccgacgagac tttggctgta aacttagctt tcaagcttta
121 tcgtgttccc gacgaaagcg tatncacgga gaatccaaga cgaacttctc cggcgcgtga
181 agggacttaa accgcgcgtg gttactctag tggagcaaga aatgaattcg aatacggcgc
241 cgttttttagg gagagtaagt nagtcatgag cgtttnacgg tgcgttnctt gantcgggtcg
301 agtctacggg tcttagtagc gatttccgac ccgtgccaaa atttnnggaa ggaatttgcc
361 cгнаanntn naaacgggt g

FIG.28A-14

atnaaaagtc tttttttttt ctttgttaca taagattcct acacttttcg aaatggaaaa
61 tcacaatgat aataatatca gaataatctc gaaaattaat aataatatgg taataataag
121 aagaaaaaaa aagagtgtgt gaagttaacg ccaagcggat gcgacagtga gtgcccgctc
181 catccaacca aagcacacac ctccgttatc ttctttaacg gtaaagcccg ggtggactcg
241 gtttccacga ctcttcacg actccgctat cttctcactc aatggcatta actcaaacc
301 agccatgctc atccgcattc gccatttncc ggaacanctc gnaccgctct atacngtcga
361 ttccttcgga cggcaccgng ttttactagc ttccggncaa ttccttctn aactttggaa
421 cggtnggatt cgttcttggt accgtaggct tggcccgtt aagaacgnac cgtacagggg
481 nntgtttnt taatttccct taaaagggg cgnnttttggg ttnatttttn ana

FIG.28A-15



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caacnntttt atagtcaagc agctctcaac gctttttttt caaggtctgt naagcctcga
61 aattatcaga ntttncaatc tccgtcgccg atgattganc tcacgtcggg gaatgatatg
121 agttnttttg gnggttcttg ttcattctcag cnttacgggt taccgggtcc cagggtctcan
181 acgcaacagc aacaatcgga ttacgggtta tttggtggga tccgaatggg aatcgggtcg
241 ggtattaata attatccaac attaaccggc gttccgtgta ttgaaccggg tcaaaaccgg
301 gttcatgaat cggaggacca ttgttganta agnttaagag agctttgtng aaacaanctt
361 tttangattg atnaccg

FIG.28A-16

tgcatacaac gcaccgtttt tcgtaacacg gtttcgcgaa gtctatttca tttctcctcg
61 atttttgaca tgcttgagac aattgtgcca cgagaagacg aagagaggat gttccttgag
121 atggagggtct ttgggagaga ggcactgaat gtaattgctt gcnaagggtg ggaaagagtg
181 gagaggcctg agacatacaa gcagtggcac gtacgggcta tgaggtcagg gttggtgcag
241 gttccatttg acccaagcat tatgaagaca tcgctgcata aggtccacac attctaccac
301 aaggattttg tgatcgggtca aagataaccg ggtggctctt tcaaggntgg aaggggaagg
361 anctgtcatg ggtctttctt ttttggaac cagagtccca aggttttncc ggaaaatcct
421 ccttgggnat ttnangnccc ttttttgtt ttttncccn gnnanttccc nggggnagtt
481 tccagtttna ggngngtttt tncnaaaa

FIG.28A-17

tgcatacaac gcaccgtttt tngtaacacg gtttcgcgaa gtctatttna tttctcctcg
61 atttttgaca tgcttganac aattgtacca cgagaagacg aagagaggat gttccttgan
121 atggagggtct ttgggagana ggcactgaat gtaattnctt gcnaagggtg ggaaagagtg
181 gagaggcctg anacatacaa gcagtggcac gtacgggcta tgaggtcagg gttggtgcag
241 gttccatttg acccaagcat tatgaagaca tcgctgcata aggtccacac attctaccac
301 aaggggtttt tgatccntcc aagataaccg gtggctcttn caaagctttg aaggggaagga
361 cttttcatgg gtcttttctt ttttggaacc aggtcccaag gtttncccg gaatccccgn
421 tggaattttg nnncccctt tgattttttt tccccgnaa tttnccc

FIG.28A-18

gagacggtag atccgncgcg ctaaagcttc ggcgaagtaa gtagccactt tnnatnagc
61 tccgggttga nacacagcta agcatccnat ttgcttcaca agagcttccg ctagagtcaa
121 attgtntcnc tggattgctt ctgcacaagc cataagcgcg tggactaaac gaacaccgtt
181 ctcttgcgag tnaaccagga taacagaacg anttgactca gccgccgcg tcgttgctgt
241 ggtggttgtc gtcaccgtcg ttcctatgac tccaccaatn tgggtaccg tcgaagtcga
301 tgtaaccata ggtacagggc ttcngcatg nttttaaaac gg

FIG.28A-19



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gtttgattcg ttggaaggag ttccgaatag tcaagacaaa gtcattntctg aagtttactt
61 agggaaacag atttgaatc nggtggcttg tnaagntcct gacagagtcg agagacacga
121 aacgttgagt caatngggaa accggtttgg ttcgtccggt ttagcgccgg cacatcttgg
181 gtctaacgag tttaagcaag cnagtatnct tttntntgtg tttaatagtg gccaagggtta
241 tcgtgtggag gagagtaatg gatgtttgat gttgggttgg cacactnngc ccactcattt
301 accacctccg gttttggaaa c

FIG.28A-20

taaaaattga tcccaaaaag gcataaatta aaaatgacct accaaaacga tatatataag
61 aatttttaaac aagtgaacga aaataaataa aataaacaaa agggaaaacg gttcgattca
121 gttcgggttta ggtcttggtc cgaacatatg tcatcaccgg tccactgac tcaatctcaa
181 attcactcgn ctcgactcca ccaccgtcgt atgcttcgag tcaaactcag tacgncgccg
241 tcgagagttt ccaagcggag gtggtaatga gtggacgagt gtgccaaccc ancatcaaac
301 atccattact ttcctccaca cgntaacctt ggccactatt taaacacagg caaaangcat
361 acttgtttgc ttaaaccgag ttagnccnaa gntttgccgg gcgntaaacc cggcngaccc
421 aanccggntt tcccnatttg ctcaaaccgg ttngtgnctt ttggcttttt gnatggcctt
481 taaangnncc

FIG.28A-21

aaaaaatggg aaaccatcac tcttgatgaa cttatgatca atccaggaga gacaacggtc
61 gtcaacngca ttcacggtt acaatacacn cctgatgaaa ctgtgtcatt agactctcca
121 agagacacgg ttctgaagct attcagagat atcaatcctg acctctttgt gttgcagag
181 attaacggaa tgtacaactc tcctttcttc atgacgaggt tccgagaagc gcttttncat
241 tacncttcac tctttgacat gtttgacacc acaatacacg gagaggatga gtacaaaaac
301 aggtcactgt ttggagagag agttactttt gaganacgag nttgagcgtg attttcctgc
361 nngggnttca nancgggtt ttngggcctt aaaacctnca agaaatnggn ggtttgggtt
421 tt

FIG.28A-22

aatcaatggt ttggttatat ttcattacta gcaaccaccc cacaaccaca tgacaattta
61 caagagaaaa acaaccacca ggtttggtt gtatacatat ataacttagg ttgtgttaca
121 acttaaaaca tcattgcaca tcctaaaaat ttcagcgacc agaattgtgt tttgattgtg
181 cctctttctt tatccacctc aagtaaccat cattcactat aacttaccca atct

FIG.28A-23



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gcgaatgttg agatcttggg agcaatagct ggggaaacca gagtccacat tatcgatttt
61 aagattgcac agggatcaca atacatgttt ttaattcagg agcttgcgaa acgccctggt
121 gggccgccgt tgctgcgtgt nacgggtgtg gatgattcan agtccaccta tgctcgtggg
181 ggaggactca gcttggtagg tgagaggctt gcaacttttg cgcagtcattg tgggtgtccc
241 ttttagtttc acgatgccat catgtctggg tgcaagggtc agcgggaaca tctcgggttg
301 gaacctggct ttgctgttgt tgtgaacttc ccatatgtat tacaccacat gccagacgag
361 agcgtaagtt tttgaaaatc acangacag gcttctgcat ctnatcaana gcctttcccc
421 aaactggtac tctagtaggc aagattcaac acaacacttg catcna

FIG.28A-24

atgnaacata tagcaaaaga tcatgcaatg agtactatat ctcttaggct acactcttac
61 acacgctatg tcacaagcat aatataacaa cattctagtg ttcaagaacc ctaactctga
121 acttaatcca ctctgtttgg cgagagacta tcaacagaaa agccctacat aatcccagt
181 cgcttagaac gtaaganaca acatctatga agacgaagga acccatagag atgaagcata
241 cacgattcta cctttccacc cttgaagtaa ccagttaccg ttttgatcaa catcgaagtt
301 tttatcgtac ccgttttcgg attttcaact tcagattctg catcagttcc ttctcaagcg
361 gnagctgtcc taaatccggg tcgggtcagt ctgggtggc actgggtata tggctctggg
421 ctctccactc tctctggtct tcacaaggca cancattcac aatctntttt ccataaaact
481 ntttttcntn catnngncnn atnttggtt ccctnggntg gttgggggnc ncnt

FIG.28A-25

tcaaggttct tctttgtcat cttgttgccg aatccacaaa gaggagaata aagattcgac
61 ctttattaga tattaacgac tctggatttt tgggtttttg gagttggatc cacatgggtt
121 cttatccgga tggattccct ggatccatgg acgagttgga tttcaataag gactttgatt
181 tgctccctc ctcaaacc aaacttaggt tagctaattg gttctattta gatgacttag
241 atttctcatc cttggatcct ccagaggcat atccctccca gaacaacanc aacaacatca
301 tcaacaacaa agctgtagca ggagatctgt tatcatcttc aactgaatga cgntggattc
361 tctgattctg ttttgagtat ataagccaag ttctnatggg agnnggtnat gnagagaagc
421 ctttgatatg tcatgnngnt ttggtgnatta agntgctngg aaannactcn ntngc

FIG.28A-26

LSMVNELRQI VSIQGDPSQR IAAYMVEGLA ARMAASGKFI YRALKCKEPP
SDERLAAMQV LFEVCPCFKF GFLAANGAIL EAIKGEEVH IIDFDINQGN
QYMTLIRSIA ELPGRPRRLR LTGIDDPESV QRSIGGLRII GLRLEQLAED
NGVSFKFKAM PSKTSIVSPS TLGCKPGETL IVNFAFQLHH MPDESVTTVN
QRDELLHMKV SLNPKLVTVV EQDVNTNTSP FFPRFIEAYE YYSAVFESLD
MTLPRESQER MNVERQCLAR DIVNIVACEG EERIERYEAA GKWRARMMA
GFNPKPMSAK VTNNIQNLIK QQYCNKYKLL EEMGELHFCW EEKSLIVASA
WR*

FIG.28A-27



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AMEGEKMHV IDLDASEPAQ WLALLQAFNS RPEGPPHLRI TGVHHQKEVL
EQMAHRLIEE AEKLDIPFQF NPVVSRLDCL NVEQLRVKTG EALAVSSVLQ
LHTFLASDDD LMRKNCALRF HNNPSGVDLQ RVLMMSHGSA AEARENDMSN
NNGYSPSGDS ASSLPSPSSG RTDSFLNAIW GLSPKVMVVT EQSDHNGST
LMERLLESY TYAALFDCLE TKVPRTSQDR IKVEKMLFGE EIKNIISCEG
FERRERHEKL EKWSQRIDLA GFGMVPLSYY AMLQARRLLQ GCGFDGYRIK
EESGCAVICW QDRPLYSVSA WRCRK*

FIG.28A-28

GTSP TGPELL TYMHILYEAC PYFKFGYESA NGAIAEAVKN ESFVHIIDFQ
ISQGGQWVSL IRALGARGPGG PPNVRITGID DPRSSFARQG GLELVGQRLG
KLAEMCGVPF EFHGAALFCT EVEIEKLGVR NGEALAVNFP LVLHHMPDES
VTVENHRDRL LRLVKHLSPN VVTLVEQEAN TNTAPFLPRF VETMNHYLAV
FESIDVKLAR DHKERINVEQ HCLAREVENL IACEGVEREE RHEPLGKWRS
RFHMAGFKPY PLSSYVNATI KGLLESYSEK YTLERDGA L YLGWKNQPLI
TSCAWR*

FIG.28A-29

AAIFYGHHHH TPPPARKLNP GPVGITEQLV KAAEVIESDT CLAQGILARL
NQLSSPVGK PLERAAFYFK EALNNLLHNV SQTLPNPSLI FKIAAYKSFS
EISPVLFQAN FTSNQALLES FHGFHRLHII DFDIGYGGQW ASLMQELVLR
DNAAPLSLKI TVFASPANHD QLELGFTQDN LKHFASEINI SLDIQVLSLD
LLGSISWPNS SEKEAVAVNI SAASFSLPL VLRVFKHLSP TIIVCSDRG
ERTDLPFSQQ LAHSLHSHA LFESLDAVNA NLDAMQKIER FLIQPEIEKL
VLDRSRPIER PMMTWQAMFL QMGFSPVTHS NFTESQAECL VQRTPVGRFH
VEKKHNSLLL CWQRTLVGV SAWRCRSS*

FIG.28A-30

KKWETITLDE LMINPGETTV VNCIHLQYT PDETSLDSP RDTVLKLFRD
INPDLFVFAE INGMYNPFF MTRFREALFH YSSLFDMFDT TIHCERRDEV
ISCEGAERFA RPETYKQWRV RILRAGFKPA TISKQIMKEA KEIVRKRYHR
DFVIDSDNNW MLQGWKGRVI YAFSCWKPAE KFTNNNLNI*

FIG.28A-31



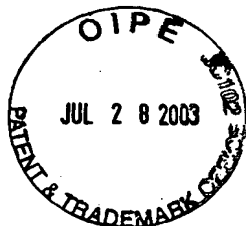
91/100

ANVEILEAIA GETRVHIIDF QIAQGSQYMF LIQELAKRPG GPPLLRVTGV
DDSQSTYARG GGLSLVGERL ATLAQSCGVP FEFHDAIMSG CKVQREHLGL
EPGFAVVVNF PYVLHHMPDE SVSVEKYRDR LLHLIKSLSP KLVTLVEQES
NTNTSPLVSR FVETLDYYTA MFESIDAARP RDDKQRISAE QHCVARDIVN
MIACEESERV ERHEVLGKWR VRMMAGFTG WPVSTSAafa ASEMLKAYDK
NYKLGGEHA LYLFWKRRPM ATCSVWKNP NYIG*

FIG.28A-32

LLKVLLCHLV AESTKRRIKI RPLLDINDSG FLGFWSWIHM GSYPDGFPGS
MDELDFNKDF DLPPSSNQL GLANGFYLD LDFSSLDPPE AYPSQNNNNN
NINNKAAGD LLSSSSDDAD FSDSVLYIS QVLMEEDMEE KPCMFHDALA
LQAAEKSLYE ALGEKDPSSS SASSVDHPER LASHSPDGSC SGGAFSDYAS
TTTTTSSDSH WSDGLENRP SWLHTPMPSN FVFQSTSRN SVTGGGGGGN
SAVYGSFGD DLVSNMFKDD ELAMQFKKV EEASKFLPKS SQLFIDVDSY
IPMNSGSKEN GSEVFKTEK KDETEHHHHH SYAPPPNRLT GKKSHWDED
EDFVEERSNK QSAVVEESE LSEMFDNMFL CGPGKPVCL NQNFPTEAK
VVTAQNGAK IRGKKSTSTS HSNDKKETA DLRTLLVLCA QAVSVDDRRT
ANVXLRQIRE HSSPLNGSE RLAHYFANSL EARLAGTGTQ IYALSSKKT
SAADMLKAYQ TYMSVCPFKK AAIIFANHSM MRFTANANTI HIIDFGISYG
FQWPALIHRL SLSRPGGSPK LRITGIELPQ RGFRPAEEFR RQVIAWLDTV
SDTMFRLSTT QLLRNGETIQ VEDLKLQGE YVVVNSLFRF RNLLDETVLV
NSPRDAVLKL IRKINPNVFI PAILSGNYNA PFFVTRFREA LFHYSAVDM
CDSKLAREDE MRLMYVFEFY GREIVNVAS EGTERVESRE TYKQWQARLI
RAGFRQLPLE KELMQNLKLK IENGYDKNFD VDQNGNWLQ GWKGRIVYAS
SLWVPSSS*

FIG.28A-33



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----- LEUCINE HEPTAD I -----
----- A ----- | ----- B -----
EVVDLRSLIHCQAQVAADRRRCAGQLLKQIRLHSTPF - GDGNQRLAHCFAANGLEARLAGTGSQIYKGT / SKP - - - - - R S A A A V L K A
ETADLRTL L L V L C A Q A V S V D D R R T A N V K L R Q I R E H S S P L - G N G S E R L A H Y F A N S L E A R L A G T G T I Y T A L S S K K - - - - - T S A A D M L K A
L S M V N E L R Q I V S I Q - G D P S Q R L A A Y M V E G L A A R M A A S G K F I Y R A L K C K E - - - - - P P S D E R L A A
T S V C S R Q T V M E I A T A I A E G K T E I A T E I L A R V S Q T P N L E - R N S E E K L V D F M A A L R S R I A S P V T E L Y - - - - - G K E - - - - - H L I S
F D L E P P L K A I Y D C A R I S D S D P N E A S K T L L Q I R E S V S E L G D P T E R V A F Y T E A L S N R L S P N S P A - - - - - T S S S S S S T E D L I L S
G P V G I T E Q L V K A A E - V I E S D T C L A Q G I L A R L N Q L S S P V G K P L E R A A F Y F K E A L N L L H N V S Q T - - - - - L N P Y S L I F K I A A
G G F G I E D L I R V V D C V E S D E L Q L A Q V L S R L N Q R L S P A G R P L Q R A A F Y F K E A L G S F L T G S N R N - - - - - P I R L S S W S E I V Q R I R A
A Q N L L S I L S N S S P H G D S T E R L V H L F T K A L S V R I N R Q Q D Q T A E T V A T W T T N E M T M S N S T V T S S V C K E Q F L R T K N N S D F E S C Y
N G V R L V H A L L A C A E A V Q K E N L T V A E A L V K O I G F L A V S Q I G - A M R Q V A T Y F A E A L A R R I Y R L S P S - - - - - Q S P I D H C L S D T L
N G V R L V H A L L A C A E A I Q N N L T L A E A L V K O I G C L A V S Q A G - A M R K V A T Y F A E A L A R R I Y R L S P P - - - - - Q N Q I D H S L S D T L
T G V R L V H A L L A C A E A V Q Q N N L K L A D A L V K H V G L L A S S Q A G - A M R K V A T Y F A E G L A R R I Y R I Y P R - - - - - D D V A S S S F S D T L
E G L H L L T L L L Q C A E A V S A D N L E E A N K L L L E I S Q - L S T P Y G T S A Q R V A A Y F S E A M S A R L L N S C L G I Y A A L P S R W - M P Q T H S L K M V S A

SCL9
SCL14
SCL1
SCL8
SCL4
SCL6
SCL15
SCL18
GAI
RGA
RGAL
SCR

----- VIIID -----
AMEGEM - - - - - V H I D L D A S E P A Q W L A L L Q A F N S R P E G - - - - - P P H L R I T G V H H Q - - - - -
H Q L F L A C C P F R K L S Y F I T N K I T I R D L V G N S Q R - - - - - V H I D F G I L Y G F Q W P T L I H R F S M Y G - - - - - S P K V R I T G I E F P Q P G F R
Y Q T Y M S V C P F K K A A I F A N H S M M R F T A N A N T - - - - - I H I I D F G I S Y G F Q W P A L I H R L S L R P G G - - - - - S P K L R I T G I E L P Q R G F R
L A E F V D L T P W H R F G I A A N A A I L D A V E G Y S S - - - - - V H I V D L S L T H C M Q I P T L I D S M A N K L H K K P - - - - - P P L K L T V I A S D A E F H P
A N V E I L E A I A G E T R - - - - - V H I I D F Q I A Q G S Q M F L I Q E L A K R P G G - - - - - P P L R V T G V D D S Q S R Y A
M H I L Y E A C P Y F K F G Y E S A N G A I A E A V K N E S F - - - - - V H I I D F Q I S Q G G W V S L I R A L G A R P G G - - - - - P P N V R I T G I D D P R S S F A
M Q V L F E V C P C F K F G L A A N G A I L E A I K G E E - - - - - V H I I D F I N Q N Q Y M T L I R S I A E L P G K - - - - - R P R L R L T G I D D P E S V Q R
T Q L L Y E L S P C F K L G F E A A N L A I L D A A D N D G G M M I P H V I D F I G E G G Y V N L L R T L S T R R N G K S Q S Q N S P V K I T A V A N N V Y G C L
Y K T L N D A C P Y S K F A H L T A N Q A I L E A T E K S N K - - - - - I H I V D F I V Q G I Q W P A L L Q A L A T R T S G K - - - - - P T Q I R V S G I P A P S L G - - - - -
Y K S F S E I S P V L Q F A N F T S N Q A L L E S F H G F H R - - - - - L H I I D F I G Y G G W A S L M Q E L V L R D N A A - - - - - P L S K I T V F A S P A - - - - -
I K E Y S G I S P I P L F S H T A N Q A I L D S L S S Q S S S P F - V H W D F E I G F G G Y A S L M R E I T E K S V S - - - - - G G F L R V T A V A - - - - -
Y L W L N Q L T P F I R F G H L T A N Q A I L D A T E T N D N G A - - - - - L H I L D I S Q G L Q W P P L M Q A L A E R S S N P S S P - - - - - P P S L R I T G C G R D V T G L -
Q M H F Y E T C P Y L K F A H T A N Q A I L E A F Q G K K R - - - - - V H V I D F S M S Q G L Q W P A L M Q A L A L R P G G - - - - - P P V F R L T G I G P P A - - - - -
Q M H F Y E T C P Y L K F A H T A N Q A I L E A F E G K K R - - - - - V H V I D F S M N Q G L Q W P A L M Q A L A L R E G G - - - - - P P T F R L T G I G P P A - - - - -
Q I H F Y E S C P Y L K F A H T A N Q A I L E V F A T A E K - - - - - V H V I D L G L N H G L O W P A L I Q A L A L R P N G - - - - - P P D F R L T G I - - - - -
F Q V F N G I S P L V K F S H T A N Q A I Q E A F E K E D S - - - - - V H I I D I M Q G L Q W P G L F H I L A S R P G G - - - - - P P H V R L T G L G T S M - - - - -

SCL3
SCL9
SCL14
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SCL8
SCL4
SCL6
SCL15
SCL18
GAI
RGA
RGAL
SCR

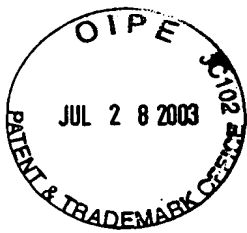
FIG.29A



----- LEUCINE HEPTAD II -----
----- A ----- B -----
----- EVLEQMAHRLIEEAEKLDIPQFNPVVSRLDCLNVEQLRVK --- TGEALAV @ DSFLNI
----- PAORVEETGOR - LAAYAKL - FGVPEFYKAIKKWDA --- IQLEDLDIDRDEITVNCIHRQLQYTPDETSLDSPRDTVLKL
----- PAEEFRROVIA - WLDTVSDTM --- FRL - STTQLRNGE - TIOVEDLKLQGEYVWVNSLFRNLLDETVLNSPRDAVKL
PPLLGISYEELGSKLVNFATTRNVAMEFRIISSYSDGLSSILQRLDPFVNEALWNCMMMLHYIPDEILTSN - LRSVFLKE
R --- GGG --- LSLVGERLATLAQSCGVPEFHDAI - MSGCK --- VOREHLGLEPGEFAVWVFPVVLHMPDESVSVEKYRDLRLHL
R --- QGG --- LELVGORLGLAEMCGVPFEFHGA - LCCTE --- VETIEKLVGRNGEALAVNFPVLHMPDESVTVENHRDLRLRL
S --- IGG --- LRIIGLRLEQLAEDNGVSFKFAMP - SKTSI --- VSPSTLGCKPGETLIVNFAQLHMPDESVTTVNQDELLHM
VD --- DGGEERLKAVGDLLSQGLRGLISVSFNVTSLRGLD --- LNRESLGCDDPDETLAVNLAFKLYRVPDESVCCTENPRDELRR
----- ESPEPSLIATGNRLRDFAKVLDLNFEPILTPHIL --- LNSSFRVDPDEVAVNFMQLYKLDET --- PTIVOTAL - R
----- NHDOLELGTQDNLKHFASEINISLDIQVLSLDLLGSTWPNSS --- EKEAVANISAA --- S --- FSHPLVLVRFVKH
----- EECAVETRLVKENLTQFAAEMKIRFQIEFVLMKTFEMLSFKAIR --- FVEGERTVWLISPA --- I --- FRRLSGITDFVNN
----- NRTGDRLTRFADSLGLOFQFHTLVIVEEDLAGLLQ --- IRLALSAVQGETIAVNCVHFLHKI --- FNDGDMIGHFL -
----- PDNFYLHEVGCKLAHLAEATHVEFEYRGFVANTLADLDASMLELRPSEISVAVNSVFLHKL --- LGRPGAIDKVLGV
----- PDNSDHLHEVGCKLAHLAEATHVEFEYRGFVANSIADLDASMLELRPSDTEAVAVNSVFLHKL --- LGRPGGIEKVLGV
----- GYSLTDIQEVGWKQLASTIGVNFEFKSIALNLSDLKPEMLDIRPGL - SVAVNSVFLHRL --- LAHGPSIDKFLST
----- PDPVQSNKLLNT
----- EA --- LQATGKRLSDFTDKLGLPFEFCPLAEKVGNLDT --- ERLNVRKREAVAVH --- WLQHS --- YDVTGSDAHTLWL

----- PFYRE -----
----- WGLSPKVMWVTEQDS --- DHNGSTLMERLLESITYAALFDCLETKVPRTSQDRIKA - VEKMLFGEEIKNII --- SCEGFER
FRDINPDLFVFAEING --- MYSPEFMTFRREALFHYSSLFDMFTTIIHADEYKNRSLERELLVRDAMSVI --- SCEGAER
IGKINPDLFVFGIVNG --- AYNAPEFVTRREALFHSSIFDMLETIVPREDEERMF - LEMEVFGREALNVI --- ACEGWER
IRKINPNVFIIPAILSG --- NYNAPFFVTRREALFHYSAVDFMCDKSLAREDEMRLM - YVFEFYGREIVNV --- ASEGTER
LRLNPTIVTLIDEDSDFTSTN NV --- AKEGAER
IKSLSPKLVTLVEQES --- NTNTSPLVSRFVETLDVYTAMFESIDAARPRDDKQRIIS - AEQHCVARDIVNMI --- ACEESER
VKHLSPNWVTLVEQEA --- NTNTAPFLPREVETMNHVLAUFESIDVKLARDHKERIN - VEOHCLAREVNLJ --- ACEGVER
VKSINPKLVTLWEQDV --- NTNTSPFFPRFIEAYEYSAVFESLDMTLPRESQERMN - VERQCLARDIVNIV --- ACEGEER
VKGLKPRWVTLVEQEM --- NSNTAPFLGRVSESCACYGALLESVESTVPSTNSDRAK - VEEG - IGRKLVNAV --- ACEGIDR
LAKLNPRWVTLGEYEV --- SLNRVGFANRVKNAQOFSAVFESLEPNLGRDSEERV - VERELFGRRISGLIGPEK --- TGIHR
L --- SPTIIVCSDRGC --- ERTDLPFSQQLAHLSHSHTALFESLDA - VNANLDMQK - IERFLIQPEIEKLV --- LDR
LRRVSPKVVFDVSEGWTSIAGSGFRFEVSALFEYTMVLESDDAAAPPGLVKKI - VEAFVLRPKISA - EATAA - DR
- SAIKSLNSRIVTMAEREAHGHDSFLNRFSEAVDHYMAIFDSLEATLPNSRERLT - LEQWFGKEILDV - AAETERKOR
VNOIKPEIFTWEQES --- NHNSPIFLDRFTESLHYSTLFDSEGV - PSQODKVM - SEVYL - GKQICNV --- ACDGPR
VNOIKPVIFTWEQES --- NHNGPVFLDRFTESLHYSTLFDSEGV - PNSQDKVM --- SEVYL - GKQICNV --- ACEGPR
IKSIRPDIMTWEQEA --- NHNGTVFLDRFTESLHYSSLFDSLEGP --- PSQDRVM --- SELF - GRQILNV --- ACEGEDR
VKAIKPSIVTWEQES --- NHNGIVFLDRFNEALHYSSLFDSLEDSYSLPSQDRVM --- SEVYL - GRQILNV --- AAEGSOR
LQRLAPKWVTLWEQD --- LSHAGSFLGRFVEATHYYSALFSDSLGASGYEESERHV - VEQQLSKEIRNVL --- AVGGPSR

FIG.29B



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----- SAW -----|

SCL3 RERHEK - LEKWSQRIDLAGFNGVPLSYAMQLARRLLQG - CGFDGYR - IKEESGCAVICWQDRPLYSVSAMRCRK
SCL11 FARPET - YKQWRVRILRAGFKPATISKQIMKEAKEIVRK - RYHRDFVI - DSDNNMMLQGWKGRVIAFSCWKPAEKFTNNNLNI
SCL9 VERPET - YKQWHVRAMRSGLVQVPFDPSPIMKTSLHKVHT - FYHKDFVI - DQDNRWLLQGWKGRVIMALSVMWKPEP
SCL14 VESRET - YKQWQARLIRAGFRQLPLEKELMQNLKLIEN - GYDKNFVDV - DQNGNWLLQGWKGRIVYASSLWVPSSS
SCL16 VERLEP FTGVGFGETAMTEVKTMLEEHATGWMKKQVDDNDVERFVLTWKGHSVMFASAWAPPN
SCL13 VERHEV - LGKWRVRMMAGFTGWPVSTSAFAASEMLKA - - KNYKL - GGHEGALYLFWKRRRPMATCSVMKPNPNYIG
SCL5 EERHEP - LGKWRSRFHMAGFKPYPLSSYVNATIKGLLES - - YSEKYTL - EERDGYALYLGWKNQPLITSCAMR
SCL1 IERYEA - AGKWRARMAGFNPMPMSAKVTNNIQNLIKQ - QYCNKYKL - KEEMGELHFCWEEKSLIVASAWR
SCL8 IERCEV - FGKWRMRMSMAGFELMPLSEKIAESMKSR - GN - RVHPGFTV - KEDNGGVCFGMMGRALTIVASAWR
SCL4 ERMEE - - KEQWRVLMENAGFESVKLSNYAVSQAKILLWNYNSLYSIVESKPGFISLAWNDLPLLTLSWR
SCL7 FGLMEE - KEQWRVLMKAGFEPVKPSNYAVSQAKLLWNYNSTLYSLVESEPGFISLAWNNVPLLTVSSWR
SCL6 SRPIERPMTWQAMFLQMGFSPVTHSNFTESQAECLVQR - TPVRGFH - VEKKNLSLLCWQRTELGVVSAMRCRSS
SCL15 RHTGE - - - MTWREAFCAAGMRPIQQSFADFQAECLLEK - AQVRGFH - VAKRQGELVLCWHGRALVATSAMRF
SCL18 HRRFE - - - - IWEEMMKRFGFVNVPIGSFALSQAKLLRL - HYSEGYN - LQFLNNSLFLGWQNRPLFSVSSW
GAI VERHET - LSQWRNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYR - VEESDGCMLMGWHTRPLIATSAMKLSSTN
RGA VERHET - LSQWGNRFGSSGLAPAHLGSNAFKQASMLLSVFNSSGQGYR - VEESNGCMLMGWHTRPLITTSAMKLSSTAA
RGAL VERHET - LNQWRNRFLGLGFKPVSIGSNAYKQASMLLALYAGADGYN - VEENEGCLLLGWQTRPLIATSAMRINRVE
SCL19 VERHET - AAQWRIRMKSAGFDP IHLGSSAFKQASMLLSL YATGDGYR - VEENDGCMLIRWQTRPLITTSAMKLA
SCR -SGEVKFESWREKMQCCGFKGISLAGNAATQATLLGMFP - SDGYTLVDDN - GTLKLGWKDL SLLTASAWTPRS

@SSVLQLHTFLASDDDLMRKNCALRFHNNPSGVDLQRVLMMSHGSAEARENDMSNNNGYSPSGDSASSLPLPSSGRT

FIG.29C

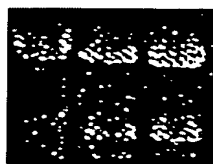
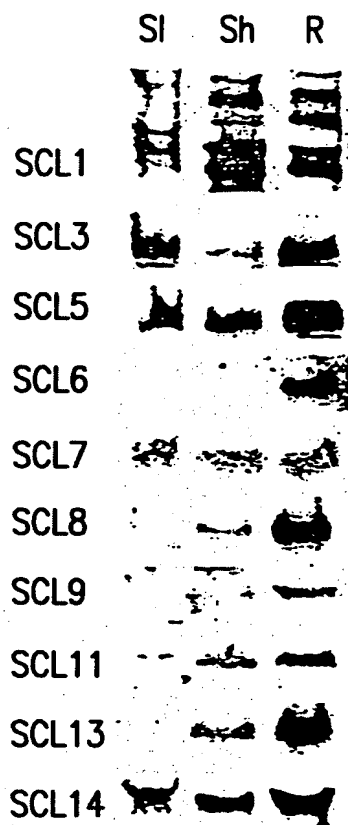


FIG.30

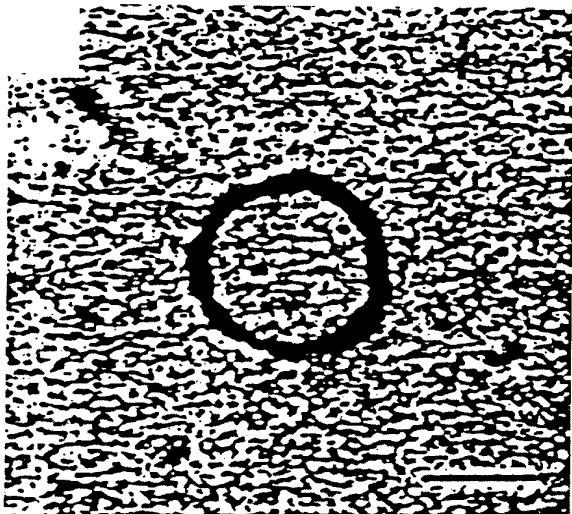


FIG. 31A

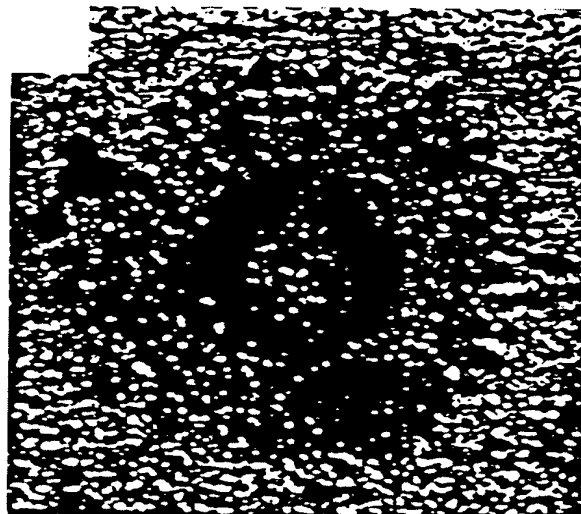


FIG. 31B



FIG. 31C

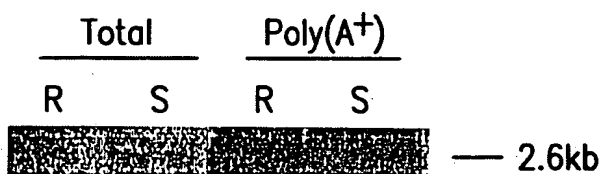


FIG. 31D



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RNA Blot Analysis



Either total RNA or poly (A⁺) RNA was probed with the full length of cDNA. About 2.6kb fragment was hybridized to the probe. R: Roots, S: Shoots

FIG.32



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CBPBT44 partial cDNA sequence

CGGGCCGCGCAGAGCCGCCGCGTGGCGGTGGCGTTCCAGGCGTACAACGCGCTGTCGCCG
CTCGTCAAGTTCTCGCACTTCACGGCCAACCAGGCCATCCTGCAGGCGCTCGACGGCGAG
GACTGCCTCCACGTGATCGACCTGGACATCATGCAGGGCCTGCAGTGGCCGGGGCTCTTC
CACATCCTCGCGTCCCGCCCCGCGCAAGCCGCGGTCTCGTCCGGATCACCGGGCTCGGCGCG
TCGCTCGACGTCTCGAGGCCACTGGCCGCCGCTCGCCGACTTCGCGGCCTCGCTCGGC
CTCCCGTTTCGAGTTCCGCCCCATCGAGGGGAAGATCGGGCACGTGCGCGACGCCGCGGCG
CTCCTCGGCTCGCGCCAGCGGCGGGGATGACGAGGCCACCGTGGTGCCTGGATGCAC
CACTGCCTCTATGACGTGACGGGGTCGGACGTGGGCACGGTGCGGCTGCTCCGGAGCCTG
CGCCCGAAGCTGATCACCATCGTGGAGCAGGACCTGGGCCACAGCGGCGATTTCTGGGC
CGGTTCGTGGAGGCGCTGCACTACTACTCGGCGCTGTTTCGACGCGCTGGGAGACGGCGCC
GGCGCGGCCGAGGAGGAGTGGCCGAGCGGTACGCGTTGAGCGACAGCTCCTGGGCGCG
GAGATACGCAACATCGTGGCCGTAGGGGGGCCCAAGCGGACAGGGGAGGTGCGCGTGGAG
CGGTGGAGCCACGAACTGCGGCACGCCGGGTTCCGGCCAGTGTCCTGGCCGGGAGCCCT
GCCGCGCAGGCCAGGCTGCTCCTCGGCATGTATCCGTGGAAGGGGTACACGCTGGTGGAG
GAGGACGCGTGCTTAAGCTGGGCTGGAAGGACCTCTCCCTGCTCACC GCGTCGGCGTGG
GAGCCGGCGGACGACGCTGCCGCTTCTGCGCCACCGGTTAACGAGTACGAGCGGACGCG
TGGGTCGAC

FIG.33A

CBPBT44 partial amino acid sequence

AAQSRRVAVAFQAYNALSPLVKFSHTANQAILQALDGEDCLHVIDLDIMQGLQWPGLF
HILASRPRKPRSLRITGLGASLDVLEATGRRADFAASLGLPFEFRPIEGKIGHVADAAA
LLGSRQRRRDDEATVVHWMHCLYDVTGSDVGTVRLLRSLRPKLITVEQDLGHSDFLG
RFVEALHYYSALFDALGDGAGAAEEESAERYAVERQLLGAIEIRNIVAVGGPKRTGEVRVE
RWSHEL RHAGFRPVSLAGSPAAQARLLLGMYPWKGYTLVEEDACLKLGWKDLSLLTASAW
EPADDAAASAPTGXRVRADAWVD

FIG.33B



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Zm SCR	GRVAAAFQVF	NGISPFVKFS
CBPBT44	RRVAVAFQAY	NALSPLVKFS
At SCR	LKMVSASFQVF	NGISPLVKFS

Zm SCR	HFTANQAIQE	AFEREERVHI	IDLDIMQGLQ	WPGLFHILAS	RPGGPPRVRL
CBPBT44	HFTANQAILQ	ALDGEDCLHV	IDLDIMQGLQ	WPGLFHILAS	RPRKPRSLRI
At SCR	HFTANQAIQE	AFEKEDSVHI	IDLDIMQGLQ	WPGLFHILAS	RPGGPPHVRL

Zm SCR	TGLGASMEAL	EATGKRLSDF	ADTLGLPFEF	CAVAEKAGNV	DPEKLGVTTR
CBPBT44	TGLGASLDVL	EATGRRLADF	AASLGLPFEF	RPIEGKIGHV	ADAAALLGSR
At SCR	TGLGTSMEAL	QATGKRLSDF	TDKLGLPFEF	CPLAEKVGNL	DTERLNVKR

Zm SCR	-----EAVA	VHWLHHSLYD	VTGSDSNTLW	LIQRLAPKVV	TMVEQDLSHS
CBPBT44	QRRRDDEATV	VHWMHHCLYD	VTGSDVGTVR	LLRSLRPKLI	TIVEQDLGHS
At SCR	-----EAVA	VHWLQHSLYD	VTGSDAHTLW	LLQRLAPKVV	TVVEQDLSHA

Zm SCR	GSFLARFVEA	IHYYSALFDS	LDASYGEDSP	ERHV---VEQ	QLLSREIRNV
CBPBT44	GDFLGRFVEA	LHYYSALFDA	LGDGAGAAEE	ESAERYAVER	QLLGAEIRNI
At SCR	GSFLGRFVEA	IHYYSALFDS	LGASYGEESE	ERHV---VEQ	QLLSKEIRNV

Zm SCR	LAVGGPARTG	DVKFGSWREK	LAQSGFRAAS	LAGSAAAQAS	LLLGMFPSDG
CBPBT44	VAVGGPKRTG	EVRVERWSHE	LRHAGFRPVS	LAGSPAAQAR	LLLGMPWKG
At SCR	LAVGGPSRSG	EVKFESWREK	MQQCGFKGIS	LAGNAATQAT	LLLGMFPSDG

Zm SCR	YTLVEENGAL	KLGWKDLCLL	TASAWRPIQV	PPCR
CBPBT44	YTLVEEDACL	KLGWKDLSLL	TASAWEPADD	AAASAPTG
At SCR	YTLVDDNGTL	KLGWKDLSLL	TASAWTPRS	

FIG.34



100/100

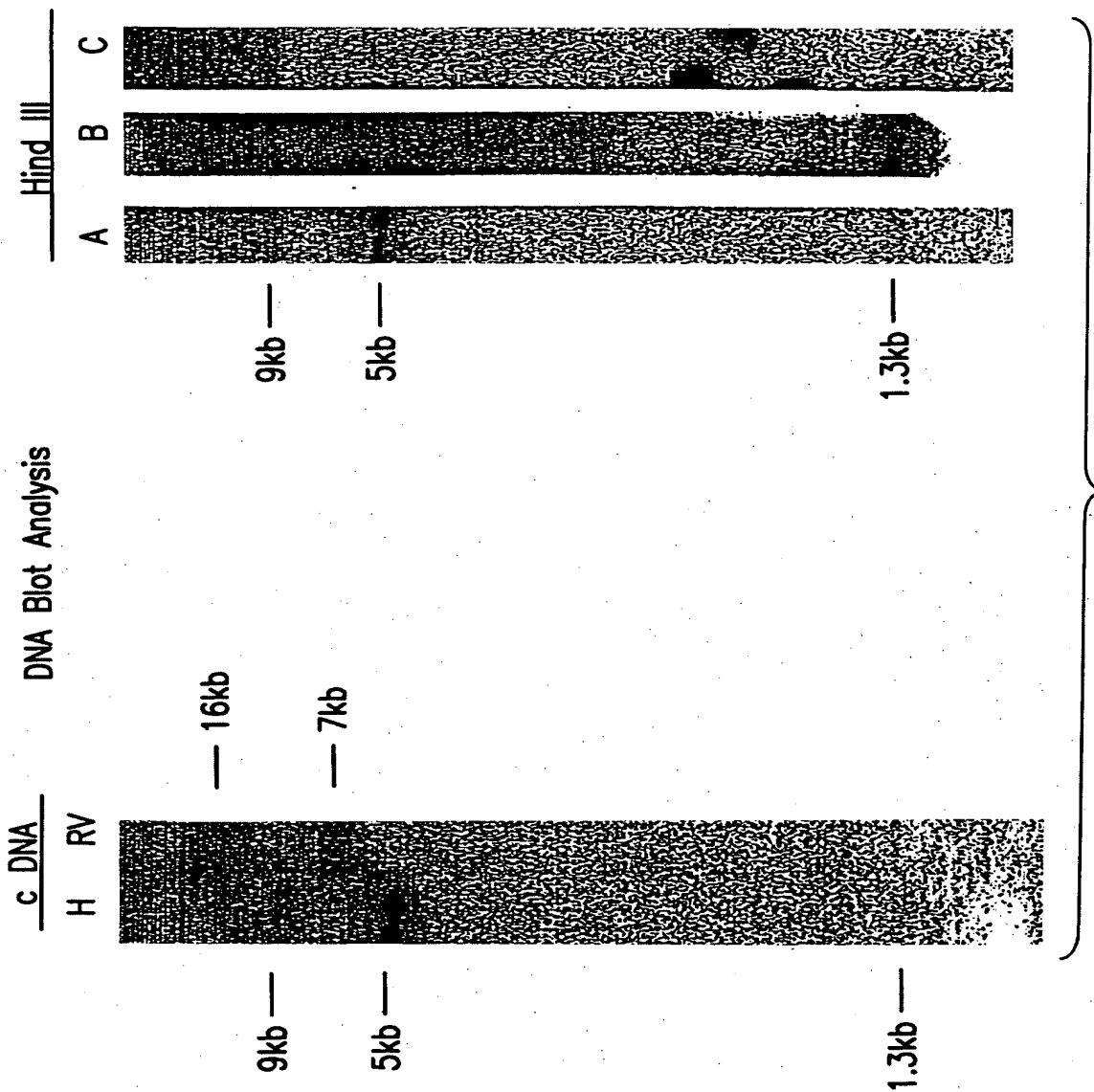


FIG.35